10-524 FOR OFFICIAL USE ONLY

204414

Scientific and Technical Information Center

SEARCH REQUEST FORM
Requester's Full Name: TANE ZALA Examiner #: 77512 Date: 10 - 12  Art Unit: 1635 Phone Number: 2-5765 Serial Number: 10/604, 72  Location (Bldg/Room#): 2018 Results Format Preferred (circle): PAPE DIS  ***********************************
To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:
Title of Invention: Bio IN FORMATICALLY DETECTABLE.
Inventors (please provide full names): Bentuich
Earliest Priority Date: 8-13-6.3
Search Topic: Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept to Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.
*For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent number, appropriate serial number.
please limit to 120 NTS.
Plene Search Seg ID Nov. 5.135, 6033, 5136 + 60
suge limit and 30 N fill tool
6033 85 na (85) 5136-24 na
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Synthetic Sequence

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OM nucleic

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Scoring table:

Searched:

Database :

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CS102090 8
AR240243 AR240243 AR100388 AR150043 BBD227916 AR211257 AR211257 AR211257 AR464547 AR4657 AR4657 AR46657 S75471 xh
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AR234292 8
AR238589 8
AR476172 8
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/mol_type="unassigned DNA"
/db_xref="txxon:32630"
/note="Computer Generated Probe Sequence."
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other sequences; artificial sequences.
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Patent: WO 0215649:-A 365 28-FEB-2002;
Illumina, Inc. (US)
Location/Qualifiers
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Sequence 4341 from Patent WO0216649.
AX447886
AX447886.1 GI:21696785
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                     AR240243
AR628705
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AUTHORS
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AX447886
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AXX15299 Sequence
AXX15300 Sequence
AXX14840 Sequence
AXX4840 Sequence
AX069252 Sequence
CS101953 Sequence
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BD141786 Novel G p
BD173668 Novel phy
BD181737 Novel G p
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AX447886 Sequence
AX538707 Sequence
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                     GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                              6366136 seqs, 31973710525 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     - nucleic search, using sw model
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AX447866
AX447866
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129861
BD1417868
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AX215297
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Gapop 10.0 , Gapext 1.0
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ggb_pat.

ggb_pt.

ggb_rt.

ggb_sts.

ggb_vt.

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Match
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Gaps

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Result

12.8 12.8

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PAT 03-JUL-2002

(CEMI-) CEMINES INC WPI; 2006-047578/05. Neuman T; 

Detecting open chromatin comprises determining hybridization of the capture probe to the treated- and untreated-sample amplification products.

Example 1; Page 37; 43pp; English.

performing a second amplification using a second portion of the chromatin sample, where the second portion is not treated with the open chromatin DNA cleaving agent, to produce untreated-sample amplification products and the open products; incubating the treated-sample amplification products with a capture probe; and the untreated-sample amplification of the capture probe; and the untreated-sample amplification of the capture probe to the products, where probe, and where reduced hybridization of the capture probe to the capture of the amplification products hybridize to the products of the capture probe to the capture probe to the untreated-sample amplification products as compared to the hybridization of the capture probe to the untreated-sample amplification products as compared to the hybridization of the capture probe to the untreated-sample amplification products indicates the presence of open chromatin in the genomic DNA. Also given is a chromatin state profiling array, for detecting the presence of open chromatin in genomic DNA. The methods and chromatin state profiling array are useful for detecting open chromatin in genomic DNA, used in diagnostic and prognostic methods, and are useful for monitoring determining the hybridization of a capture probe to a treated sample amplification products and the untreated sample amplification products. Specifically, the method comprises preparing a chromatin sample from cells, the chromatin sample comprising genomic DNA segments or genomic DNA with one or more open chromatin sites; treating a first portion of the chromatin sample with an open chromatin DNA cleaving agent to produce fragments; performing a first amplification reaction using the fragments as a substrate, to produce treated-sample amplification products; are useful for uscenting year commenced and are useful for monitoring diagnostic and prognostic methods, and are useful for monitoring treatment and evaluating the response of cells and patients to candidate to care this the present sequence is a 3' reverse open chromatin in genomic DNA by chromatin or established therapeutic agents. The present sequence is a primer for one-sided PCR amplification of DNase I treated chr fragments, deposited on a chromatin profiling array new invention relates to detecting

Sequence 25 BP; 13 A; 0 C; 11 G; 1 T; 0 U; 0 Other

ö 65.0%; Score 15.6; DB 15; Length 25; 40.9%; Pred. No. 4.5e+03; ive 9; Mismatches 4; Indels ( 4 9; Conservative Query Match Best Local Similarity Matches 9; Conserv

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Gaps

g 8

RESULT 10 

BP. ADI94591/c ID ADI94591 standard; DNA; 21

(first entry) 04-NOV-2004 ADI94591;

Murine IFN-gamma associated probe SEQ ID 2144.

functional domain; nucleic acid cleavage assay; nuclease; polymerase;
detection; microorganism; RNA genome; hepatitis C;
human immunodeficiency virus; ss; probe.

Mus musculus.

WO200190337-A2

29-NOV-2001

24-MAY-2001; 2001WO-US017086

2001US-00758282 2001US-00864426 24-MAY-2001; 2001US-00864636 24-MAY-2001;

(THIR-) THIRD WAVE TECHNOLOGIES INC.

Hall JG; V, Ma W; Takova TY; Bartholomay CT, Chehak L, Curtis ML, Bis PS, ser M, Kwiatkowski RW, Lukowiak AA, Lyamichev Schaefer JJ, Skrzypczynski Z, Neri BP; Allawi H, Bartholomay CT, Ip HS, Kalser M, Kwiatkowe Olson-Munoz MC, Olson SM, Lyamichev NE, vedvik KL,

WPI; 2002-083110/11.

RNA Composition comprising enzyme which comprises heterologous functional domain that provides altered functionality in nucleic acid cleavage assay, useful for cleaving nucleic acid, and detecting presence of RNA target

Claim 95; SEQ ID NO 2144; 1266pp; English

the maturally occurring polymerase. Preferably the polymerase is a thermostable polymerase from a Thermus species such as T. aquaticus, T. flavus, T. socoductus. The enzyme comprises a heterologous functional domain, an amino acid sequence that provides an improved substrate binding activity in the nucleic acid cleavage assay and an amino acid sequence that provides improved background specificity in the nucleic acid cleavage structure comprises a RNA target nucleic acid (a cytochrome packground specificity in the nucleic acid (a cytochrome cleavage structure comprises a RNA target nucleic acid (a cytochrome generates an non-target cleavage of the invasive cleavage structure cleavage product, which is then detected by detecting fluorescence, mass or fluorescence energy transfer or by detecting radioactivity luminescence, phosphorescence, fluorescence polarisation or charge. The enzyme which for cleaving a nucleic acid to the enzyme which produces at least one detectable cleavage product. The enzyme which produces at least one detectable cleavage product. The enzyme which produces at least one detectable cleavage product. The enzyme which produces at least one detectable cleavage of the mans, other animal or plants that are or may be associated with the animal or mans, the craft of the product or may be associated with This invention describes a novel composition comprising an enzyme which contains a heterologous functional domain that provides altered functionality in a nucleic acid cleavage assay. The enzyme comprises a 5' nuclease, preferably a thermostable 5' nuclease, or a polymerase which is altered in sequence related to a naturally occurring sequence of a polymerase such that it exhibits reduced DNA synthetic activity from that

disease or other conditions. In addition, the enzymes may be useful for detecting and identifying strains of microorganisms including bacteria, fungi, protozoa, ciliates and viruses, preferably detecting and identifying viruses having RNA genomes, such as hepatitis C and human immunodeficiency virus 

Sequence 21 BP; 9 A; 3 C; 8 G; 1 T; 0 U; 0 Other;

Length 21, 3; Indels Score 15.2; DB 7; Pred. No. 6.6e+03; 63.3%; Scor. 50.0%; Pred. No. e... 7; Mismatches Query Match
Best Local Similarity 50.v.
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ADI94589 standard; DNA; 22 RESULT 11 ADI94589,

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ADI94589; XXXEXEX XEXEXEX

04-NOV-2004 (first entry)

Murine IFN-gamma associated probe SEQ ID 2142.

Oligonucleotide array; adapter sequence; probe; ss.

27-AUG-2001; 2001WO-US026519

WO200216649-A2.

Synthetic.

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Gaps

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28-FEB-2002

2000US-0227948P 2000US-0228854P

25-AUG-2000; 29-AUG-2000;

(ILLU-) ILLUMINA INC

Oligonucleotide adapter/capture probe 12529.

11-JUN-2002

ABQ12538;

ABQ12538 standard; DNA; 25 BP

RESULT 12

ABQ12538

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nucleic acid sequence by attaching a adapter nucleic acid (AB000010-AB013409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (1). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid.
                                                                                                                                                / Match 18.6%; Score 15.8; DB 6; Length 24; Local Similarity 73.7%; Pred. No. 5.9e+04; tes 14; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide array; adapter sequence; probe; ss.
                                                                                                             Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
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ID ABQ11043 standard; DNA; 24 BP.
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29-AUG-2000; 2000US-0228854P.
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                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. [I) is useful for immobilising a target nucleic acid sequence by attaching a adapter imclaic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
                                                                                                                                                                                                                                                                                                                               Array comprising adapter sequences useful for immobilizing or detecting target nucleic acid sequence, has different addresses comprising different specific capture probes.
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Pred. No. 6e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
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Best Local Similarity 73.7%;
Matches 14; Conservative
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ABQ12579 standard; DNA; 25
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WO200216649-A2

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Gaps

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DB 6; Length 24;

18.6%; Score 15.8; DB 6; Length 2 73.7%; Pred. No. 5.9e+04; ive 3; Mismatches 2; Indels

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Best Local Similarity 73.7 Matches 14; Conservative

Query Match

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OM nucleic

Run on:

Sequence:

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AR340859 Sequence
AR128827 Sequence
AR126073 Sequence
AR473711 Hepatitis
BD270121 Method of
C0534358 Sequence
X14934 Mouse mRNA
M18023 Human DNA t
C0080813 Sequence
C0115279 Sequence
C0115279 Sequence
C0115279 Sequence
C0214971 Sequence
C0237346 Sequence
C0237346 Sequence
C0237345 Sequence
C0237345 Sequence
C0249319 Sequence
AX92571 Sequence
AX92571 Sequence
AX92573 Sequence
AX236505 Sequence
AX36537 Sequence
AX395943 Sequence
AX39543 Sequence
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
Patent: WO 014467-A 193 14-JUN 2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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Sequence 193 from Patent WO0142467.
AX184498
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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CS254876
AR126073
AF473711
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MMTRB138
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AX992971
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AR166135
AR235763
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      Homo sapiens (human)
      Hominidae; Homo
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      69
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Matches 26;
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SOURCE
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AY753641 Sus scrof
AR165723 Sequence
AR304919 Sequence
BD034273 Sequence
AR734534 Sequence
AX898740 Sequence
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AX987628 Sequence
BD122487 EST and e
AR426934 Sequence
E08253 linker. 9/1
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E08252 linker. 9/1
AXI84576 Sequence
BX294351 Arabidops
A86879 Sequence 19
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BD070385 Factor X-
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                       GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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AR165723
AR304919
BD034273
AR334534
AX388740
EWU12530
E08252
AX184576
BX294351
AG6879
BD070385
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     nucleic search, using sw model
                                                                                                                                              October 16, 2006, 14:22:20
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AX772410
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E08253
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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seg length: 100
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Perfect score:
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homonindae; Homo.

1 (bases 1 to 93)
Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
Partant encoded human protein
Patent: JP 2002010789-A 14564 15-JAN-2002;
                                                                                                         OS Homo sapiens (human)
PN JP 2002010789-A/14564
PD 15-JAN-2002
PF 07-AUG-1999 US 60/147499
PR 05-AUG-1999 US 60/147499
GIORDANO
PC C12N15/09,C12N18/No CANTAL
                                                                                                                                                                                                                                                                                   C12N1/21,
PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00,
C12N15/00
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Unclassified.
Unclassified.
1 (Dases 1 to 93)
Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 18431 28-OCT-2003;
Genset S.A.;;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="unknown"
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Matches 23; Conserva
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                                                      REFERENCE
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E08253/c
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhin;
                                                                       Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                             Dickson, B., Berger, J., Suzuki, T. and Knoblich, J.
Method for identifying therapeutic targets by use of genetic screens in drosophila melanogaster
Patent: WO 30344547-A 200 22-MAY-2003,
BOEHRINGER INGELHEIM INTERNATIONAL GMBH; CD Patents (DE)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
/mol_type="unassigned DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                           ch 25.6%; Score 20.2; DB 2; Il Similarity 51.5%; Pred. No. 2.3e+04; 17; Conservative 8; Mismatches 8;
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Patent: EP 1104808-A 18431 06-JUN-2001;
Genset (FR)
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Sequence 18431 from Patent EP1104808.
AX987628
AX987628.1 GI:40993768
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     Sequence 200 from Patent WO03042407.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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EST and encoded human protein.
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JP 2002010789-A/14564.
Homo sapiens (human)
Homo sapiens
                         AX772410
AX772410.1 GI:32438983
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Best Local Similarity
Matches 17; Conserva
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AX987628/c
LOCUS
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ACCESSION
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BD122487/c
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PAT 17-0CT-2001
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<1. .>92
/gene="CRBB"
/codo="CRBB"
/codo="CRBB"
/procduct="CAMP response element binding protein"
/procein_id="AAV30667.1"
/db.xref="C41.54125966"
/translation="APTVTLVQLPNGQTVQVHGVIQAAQPSVIQS"
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Parma,D.H., Hicke,B., Bridonneau,P. and Gold,L.
High affinity nucleic acid ligands to lectins
Parent: US 6280932-A 288 28-AUG-2001;
Location/Qualifiers
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Parma, D.H., Hicke, B., Bridonneau, P. and Gold, L. High affinity nucleic acid ligands to lectins Parent: 108 6544959-A 288 08-APR-2003; Gilead Sciences, Inc.; Foster City, CA Location/Qualifiers
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Sequence 288 from patent US 6280932.
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/mol_type="unassigned DNA"
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AR165723.1 GI:16240708
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                                                                                                               <1. .>92
/gene="CREB"
/number=4
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                                                                                                                                                                                                                            23; Conservative
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Unclassified.
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Matches 19; Conserva
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Best Local Similarity
Matches 23; Conserv
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AR304919/c
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Submitted (20-SEP-2004) Department of Animal Genetics and Breeding,
Agricultural University of Poznan, Wolynska 33, Poznan 60-637,
Poland
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                           C07K13/00, A61K37/02, C12N1/21, C12N5/10, C12N15/12, C12N15/70, PC
                                                                                                                                                                                                                                                         25-NOV-1991 JP 1991308976
30-NOV-1990 JP 90P 335720, 25-FEB-1991 JP 91P 30271 PI
TAKESHI, IWASAKI AKIO, SAINO SUKEYUKI, KIMURA SHIGERU, PI
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                                                                                                                           Doi,T., Iwasaki,A., Saino,S., Kimura,S. and Oguchi,M.
THROMBIN-BINDING SUBSTANCE AND ITS PRODUCTION
Patent: JP 1994279497-A 12 04-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism='Artificial sequences'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 63;
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strandedness: Single;
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Pred. No. 3.4e+04;
4; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers

    . .63
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

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/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
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Chmurzynska, A. and Switonski, M.
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JP 1994279497-A/12
04-OCT-1994
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                                                                                              unclassified sequences
                                                                                                                                                                                                                                                                                                                                                                                            topology: Linear;
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Local Similarity 59.0%;
nes 23; Conservative
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                                GI:2176374
                                               JP 1994279497-A/12
                                                                                                               (bases 1 to 63)
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Sus scrofa
                                                                                                                                                                                                          OC Artificia
PN JP 1942
PN JP 1942
PF 25-NOV-11
PR 30-NOV-11
DOI TAKESH,
OGUCHI MASAO
PC COTK13/02,
PC (C12N1/2)
CC Strandedi
CC Strandedi
CC STRANDEDI
FH KEY
FH KEY
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Homo sapiens (human)
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012530.1 GI:902953
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PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
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I (basea I to 51)
Edwards, J. B.D.M., Duclair, E. and Jordan, J. Y.
Sequence tag and encoded human protein
Parent: JP 2001269182-A 10519 02-OCT-2001;
                                                                                                                31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-0CT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
                                                                                                      GTGAGCCTCCTGTCGAATCTTACTACTTCTGCTTTGTGTTTTGTTTCCTTGCGTGCCCCTT
                                                                                     GAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUCGCCACCUC
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                             24.6%; Score 19.4; DB 2; Length 97; ilarity 31.1%; Pred. No. 5.1e+04; Conservative 16; Mismatches 26; Indels
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1 (bases 1 to 51)
Edwards,J.-B.D.M., Duclert,A. and Giordano,J.-Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGAGGCGGGGGAGAGACGAGCGGCUCUGGCCCCUUAAUU 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers.
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                                                                                                                                                                                                                                            Sequence tag and encoded human protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
JP 2001269182-A/10519
                                                                                                                                                                                                                                                                                        BD034273.1 GI:22576015
JP 2001269182-A/10519.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity
Matches 24; Conservat
                                         Best Local Similarity
Matches 19; Conserv
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AR734534/c
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AUTHORS
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100 bp mRNA linear ROD 21-JUL-1995
Rattus norvegicus ultraviolet B radiation-activated UV126 mRNA,
partial sequence.
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Rosen, C.F., Poon, R. and Drucker, D.J.
Ultraviolet B radiation-activated genes induced by transcriptional and posttranscriptional mechanisms in rat keratinocytes
Unpublished
2 (bases 1 to 100)
Rosen, C.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Sukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
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Expressed sequence tags and encoded human proteins
Patent: EP 1033401-A 14603 06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 24.3%; Score 19.2; DB 2; Length 51; Best Local Similarity 60.0%; Pred. No. 5.4e+04; Matches 24; Conservative 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                 51,
Expressed sequence tags and encoded human proteins Patent: US 6783961-A 14603 31-AUG-2004; Genset S.A.;; FRX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Best Local Similarity 60.0%; Pred. No. 5.4e+04;
Matches 24; Conservative 3; Mismatches 13
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    .51
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/db_xref="taxon:9606"

                                                                                                                                                                            /mol_type="genomic DNA"
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PAT 06-AUG-2001

linear

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                      Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer. Patent: WO 0142467-A 271 14 JUN-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 24.1%; Score 19; DB 2; Length 65; 1 Similarity 37.5%; Pred. No. 6.7e+04; 15; Conservative 10; Mismatches 15; Indels
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                                                                       65 bp C
Sequence 271 from Patent WO0142467.

    .65
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Job time : 1301 secs
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AX184576.1 GI:15135934
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Best Local Similarity
Matches 15; Conserv
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AX184576/c
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Submitted (21-JUL-1994) Cheryl F. Rosen, Medicine, University of Toronto, 100 College Street, Room 317, Toronto, Ontario, MSG 1L5, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-NOV-1991 JP 1991308976
30-NOV-1990 JP 90P 335720, 25-FEB-1991 JP 91P 30271 PI
TAKESHI, IWASAKI AKIO, SAINO SUKEYUKI, KIMURA SHIGERU, PI
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Location/Qualifiers
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Doi.T., Iwasaki.A., Saino,S., Kimura,S. and Oguchi,M.
THROMBIN-BINDING SUBSTANCE AND ITS PRODUCTION
PREDAT: JP 1994279497-A 11 04-OCT-1994;
KOWA CO
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                                                                                     /organism="Rattus norvegicus"
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/clone="UV126T7"
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 1994279497-A/11
04-OCT-1994
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JP 1994279497-A/11.
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C12P21/02,
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Result

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New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with
                                                                                                                                                                                                                                                                                                               Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                               Human cervical cancer marker nucleic acid 193.
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                                                  ABA74927
AA155452
ABA39617
AAK49572
AAK33422
ABS33058
ABS3058
ABS3058
ACC73164
ACC73164
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ADP49484
AAL24704
AAL24473
ABK36475
AAH71852
AAH68985
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ADU25177
ADU22644
                             ABN31245
ADM95117
      AAF70953
AAT00367
AAA09070
                                            AAI26680
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21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189315P.
                                                                                                                                                                                                                                                                                                                                                                                                            12-MAY-2000; 2000US-0203791P.
09-JUN-2000; 2000US-0210600P.
21-JUL-2000; 2000US-0220114P.
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9426914
                                                                                       AAH68919 standard; cDNA; 97
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                              Schlegel R, Deeds J,
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WO200142467-A2.
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AAH68919;
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Abg79817 W. capgul
Abd19391 Human RAN
Ada22018 HGF aptam
Adc10528 Human sec
Adm79864 DNA ligan
Abx51458 Bovine ES
Aah68997 Human Cer
Adx69632 Human GnT
Adx69632 Human GnT
Adx69632 Human GnT
Adx69637 Schizosac
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Aax54100 RANTES re
Aaa33544 Low adeno
Aaf19666 Human MIP
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Abl75509 Corn tass
                                                          alignments)
Million cell updates/sec
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ABL75509
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cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                                                                                                                                                                                                                                75
                                                                                                                                                                                                                                                                                                                                                                                               purified corn tassel-derived polynucleotide useful for determining
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                                                                                                                                                                                                                                                                                                                                                                16 GACGAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCCUUUCGCCAC
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                                                                                                                                                                                   Sequence 97 BP; 7 A; 34 C; 30 G; 23 T; 0 U; 3 Other;
                                                                                                                                                                                                                                           29.9%; Score 23.6; DB 4; 40.6%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                     12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sherman BK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL75509 standard; cDNA; 87 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0082567P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                     26; Conservative
                                                                                                                              useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LALGUDI R V.
ITO L Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LALG/) LALGUDI R V. (ITOL/) ITO L Y. (SHER/) SHERMAN B K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lalgudi RV, Ito LY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-163647/21.
                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 CUCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 ၁၁၅၁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-DEC-2001
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                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL75509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel
                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
ABL75509/C
ANC ABL7509/C
ANC
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                                                                                                                                                                                                                                                                                                                    9 GGGGAGAGACGAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUU 68
                                                                                                                                                                                                                                                                                                                                                 73 GGGGNGAGTCCGCTGGNAGTTNCCCATGAANNCTATNTNGANCTCGCTCGACCTCGCCGA 14
clone regulatory elements for use in transformation vectors, to express polypeptide, to identify, isolate or extend identical or related corn tassel nucleic acid sequences from DNA libraries, in nucleic acid hybridisation or amplification technologies, as query sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary bypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;
                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                   Score 23; DB 6; Length 87;
Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                               33; Indels
                                                                                                                                                                                             Seguence 87 BP; 17 A; 22 C; 23 G; 15 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RANTES receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 53; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0059160P.
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                                                                                                                                                                                                                                     ch 29.1%;
1 Similarity 43.7%;
31; Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX54100 standard; DNA; 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          69 UCGCCACCUCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                   13 ACGTCAGCTCC 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate cancer; ss
                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vasoconstriction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                          ведпепсев
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX54100;
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conditions or mixtures. The antisense oligonucleotides may be derived from sequences AX55219-74. These multiple target oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, including lung diseases, pulmonary vasoconstriction, impeded respiration, respiratory bulmonary vasoconstriction, emphysem, chronic obstructive pulmonary disease (COPD), and cancer such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, pepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer
                                                                                                                                                                                                                                                                                                                          GGGCGGGGGAGAGAGCGGCCCCCCUAAUUGUACUCGGGCCCGUAUUGUCUC 63
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; adenosine receptor; low adenosine antisense oligonucleotide;
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                                                                                                                                                                                                                                                             ch 25.8%; Score 20.4; DB 2; Length 86; I Similarity 38.6%; Pred. No. 2.9e+03; 27; Conservative 17; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Low adenosine antisense oligonucleotide SEQ ID NO:1233.
                                                                                                                                                                                                                               Sequence 86 BP; 0 A; 26 C; 26 G; 19 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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61 CCCBTBGTC 70
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Best Local Similarity
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antiallergic, antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss. Homo sapiens

99WO-US017712 98US-0095212P (UYEC-) UNIV EAST CAROLINA. WO200009525-A2 03-AUG-1999; 03-AUG-1998; 24-FEB-2000.

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers

WPI; 2000-205971/18.

Nyce JW;

24-MAR-2000; 2000WO-US008020.

WO200062736-A2.

26-OCT-2000.

Homo sapiens.

cancer;

99US-0127958P.

06-APR-1999;

(UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.

Claim 18; Page 419; 1343pp; English.

The present invention describes a new composition comprising an antisense

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coligonucleotide (ON) with low adenosine (up to 15%), which targets
nucleic acids involved in bronchoconstriction, allergies, and/or
inflammation. The ON can have antiinflammatory, antiallergic,
antiasthmatic, cytostatic and analogesic activities. The compositions are
useful for the treatment of diseases associated with inflammation,
impaired airways, including lung diseases and diseases whose secondary
c effects afflict the lungs of a subject. They can be used for treating
c e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
impeded respiration, respiratory distress syndrome, pain, cystic
fibrosis, pulmonary hypertension, emphysema, chronic obstructive
c pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
carcinomas, and cancers which may metastasise to the lungs, including
breast and prostate cancer. The reduction of the adenosine content of the
c ONS reduces side effects. The A-containing ONS break down with the
crolease of deoxyadenosine which activates adenosine receptors causing
c bronchoconstriction and inflammation. AAA33312 represent the
c nucleotide sequences given in the sequence listing from the present
c invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
c sequences are also called SEQ ID NO:1 to 185, but the sequences of from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
AAA3392) are specifically claimed ONS from the present invention. N.B.
c AAA3392) are specifically claimed ONS from the present invention. N.B.
c AAA3392) are specifically claimed on the present invention. N.B.
c AAA3392) are specifically claimed on the present invention. N.B.
c AAA3392) are specifically claimed on the present invention. N.B.
c AAA3392) are specifically claimed on the present invention. N.B.
c AAA33920 and the present invention of the present invention and the present invention of the present invention and the present invention of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GGGCGGGGGAGAGACGACCGCUCUGGCCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with their corresponding SEQ ID NO: sequences given in the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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1 Similarity 38.6%; Pred. No. 2.9e+03; 
27; Conservative 17; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 86 BP; 0 A; 26 C; 26 G; 19 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human MIP-1-alpha/RANTES receptor DNA fragment #1233.
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61 CCCCBTBGTC 70
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Homo sapiens.

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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antinflammatory, analgesic, immunosuppressive, antiasthatic, bronchodilator, antinflammatory, analgesic.

(I) can have respiratory, bronchodilator, antinflammatory, analgesic, immunosuppressive, antiasthatic, such as stimulating cativities.

(I) can have respiratory disorders and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with activating peptide factors and transmitters, transcription factors, immunoslobulina and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adenosine receptors, bradykinin receptors, central nervous and non-nervous system peptide receptors, adenosine receptors, bradykinin receptors, central creceptors, defensins, growth factors, bradykinin receptors, central creceptors, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction cand/or bronchoonstriction) which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, or suffactant hypoproduction which are associated with a disease or allegines, asthma, impeded respiration, respiratory distress syndome or one allegines, sthmation, expiration, respiratory is trained by any minmary ones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                          Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiatethmatic; hypotensive; immunosuppressive; cycostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GGGCGGGGGAGACGACGGCCCCCUVAAUUGUACUVCGGGCCVCGUAUUGUCCC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantention rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.8%; Score 20.4; DB 3; 38.6%; Pred. No. 2.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.6%; Prec. ...
tive 17; Mismatches
                                                                                                                                                                                                                                 Claim 14; Page 219; 1592pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ95360 standard; DNA; 86 BP.
                                                                                                                                                                                   and respiratory obstructions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 38.6%
....hes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention
                                                                         WPI; 2000-679539/66.
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                           Nyce JW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RDS)
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Open circle probe; rolling circle replication primer; mutation detection; amplification target circle; unimolecular segment amplification; multiple target detection; circular DNA; human; cystic fibrosis; ss.
                          4 GOGCOGOGGAGACGAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUC 63
                                           0; Gaps
                                                                                                                                                                                                                                                                                   Open circle probe for cystic fibrosis gene.
                                                                                                                                                                                               Bb
                                                                                                                                                                                            AAT69848 standard; DNA; 90
                                                                                                                                                                                                                                                       (first entry)
                                                                                                          61 CCCCBTBGTC 70
                                                                                        64 UCCUUUCGCC 73
                                                                                                                                                                                                                                                       05-MAR-1998
                                                                                                                                                                                                                             AAT69848;
                                                                                                                                                                                AAT69849
ID AAT6
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AC AAT6
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonuclectide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, 7' or 2' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nuclectides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in a prophylactic or therapeutic respiratory effect of an antisinflammatory steroid in a subject; for reducing or depleting levels of or receptor, producing bronchodilation, increasing levels of adenosine creceptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Once: The sequence data for this patent is not represented in the printed producing allergies, or a respiratory disease or condition.
                                                                                                                                                                                                                                                                                                                                                                                                                         Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                    Katz E, Pabalan J, Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.8%; Score 20.4; DB 10; Length 86; Best Local Similarity 38.6%; Pred. No. 2.9e+03; Matches 27; Conservative 17; Mismatches 26; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 86 BP; 0 A; 26 C; 26 G; 19 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 10602; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                       Li Y, Sandrasagra A, K
Tang L, Shahabuddin S;
                                                                                                                                                   23-APR-2002; 2002WO-US013135.
                                                                                                                                                                                                   24-APR-2001; 2001US-0286137P.
                                                                                                                                                                                                                                                     (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-229219/22
                                                                                                                                                                                                                                                                                                       Li Y,
                                                  WO200285308-A2
                                                                                                    31-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ubiquinone.
                                                                                                                                                                                                                                                                                                                                    Miller S,
                                                                                                                                                                                                                                                                                                       Nyce JW,
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Human, antisense, bronchoconstriction, allergy, hyposecretion, pain, respiratory tract inflammation, adenosine sensitivity, lung, cancer; surfactant depletion, antiallergic, antiliflammatory; antiasthmatic; analgesic; hypotensive; lmmunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; pulmonary hypertension; pulmonary transplantation rejection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           M. capsulatus, and for studying gene expression on a genomic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ABQ9016-ABQ91855 represent M. capsulatus genes for use in arrays of the
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel DNA array giving a representation of a number of Methylococcus capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of
                                                                                                                                                                                                                                                      Novel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus
                                                                                                                                      Eidhammer I, Jonassen I, Jensen HB, Lien T;
Lossius I, Eisen JA, Fraser CM, Durkin AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.1%; Score 19.8; DB 6; Length 93; 51.6%; Pred. No. 4.8e+03; ative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 93 BP; 17 A; 30 C; 26 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Katz E, Pabalan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 eccacerrrrrcacrcerrreeracece 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 GCUCGUAUUGUCUCUCCUUUCGCCACCUCC
                                                                          UNIF-) UNIFOR STIFTELSEN UNIV BERGEN
                                                                                                                                                                                                                                                                                                                                                       Claim 14; Page 359; 678pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li Y, Sandrasagra A, K
Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human RANTES DNA fragment 1224.
                  12-JAN-2001; 2001NO-00000235
12-JAN-2001; 2001NO-00000239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2002; 2002WO-US013143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-2001; 2001US-0286036P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                  Eidhammer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABD19391 standard; DNA; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 51.6
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::
                                                                                                                                                                                                                   WPI; 2002-557818/59.
                                                                                                                                                                                                                                                                                                                      capsulatus genes.
                                                                                                                                                     Lillehaug JR,
Salzberg SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200285309-A2
                                                                                                                                      Birkeland NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nyce JW, 1
Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABD19391;
                                                                                               (TIGR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABD19391
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a probe to test the method of the invention. The method of the invention is for amplifying a nucleic acid molecule. It comprises mixing at least one rolling circle replication primer (RCRE) with at least one amplification target circle (ATC) which comprises a single stranded circular DNA containing a region complementary to the CRCRP, such that the RCRP hybridises to the ATC and mixing the ATC-RCRP complex with a DNA polymerase and incubating such that a tandem sequence DNA is formed. The method, designated unimolecular segment amplification, is used for detecting specific sequences with high speed and sensitivity. It is especially useful for detecting mutations in genes where numerous distinct mutations are associated with a disease or where mutations in multiple genes are involved. The method is isothermal and provides a simple, consistent amplification occurs not in cycles but as a single continuous reaction. The method is strictly quantitative as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                        Unimolecular segment amplification method for amplifying nucleic acids -uses rolling circle mechanism of amplification, useful for disease-associated genetic mutation(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amplification step is linear and is catalysed by a highly processive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Micro array; gene; ds; differential expression; gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 90 BP; 24 A; 18 C; 12 G; 36 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 CCUUNAUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUCG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 25.1%; Score 19.8; DB 2;
1 Similarity 35.9%; Pred. No. 4.8e+03;
14; Conservative 13; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. capsulatus gene #802 for DNA array.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 82; 149pp; English.
                                                                                                                                                       96WO-US018812.
                                                                                                                                                                                              95US-00563912.
96US-0016677P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JAN-2002; 2002WO-NO000019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ90817 standard; DNA; 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methylococcus capsulatus
                                                                                                                                                                                                                                                                                               Caplan M;
                                                                                                                                                                                                                                                                                                                                     WPI; 1997-298125/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                      (UYYA ) UNIV YALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200255655-A2.
                                   Homo saplens
                                                                        WO9719193-A2
                                                                                                                                                     21-NOV-1996;
                                                                                                                                                                                                                 01-MAY-1996;
                                                                                                                                                                                            21-NOV-1995;
                                                                                                                                                                                                                                                                                               Lizardi PM,
                                                                                                               29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUL-2002
                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ90817;
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Gaps

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Aguilar D;

Gold L;

Janjic N,

91US-00714131. 95US-00469609. 95US-00536428. 99US-00364539.

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antiarthritic; gene therapy; cytostatic; RNA aptamer; hepatocyte growth factor/scatter factor; HGF; HGF receptor; c-met; ligand; tumour; angiogeneals; vascular endothellal factor; VGF; basic fibroblast growth factor; hypertension; arteriosclerosis; myocardial infarction; rheumator; hypertension; acteriosclerosis; systematic evolution of ligands by exponential enrichment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA22018 standard; RNA; 97 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 24.8%;
Best Local Similarity 38.6%;
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CCCCNTNGTC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 UCCUUUCGCC 73
                                                                                                                                                                   bronchodilating agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA22018;
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AC ADA2:

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New nucleic acid ligands to hepatocyte growth factor/scatter factor or c-met, diagnostic and therapeutic agents for hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          met, diagnostic and therapeutic agents for hypertension, arteriosclerosis, myocardial infarction and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 101; 157pp; English.
                                                                                                                                                    04-FEB-2002; 2002US-00066960
                                                                                                                                                                                                                                                                                                             10-FEB-2000; 2000US-00502344
                                                                                                                                                                                                                                                                                                                                                                (GILE-) GILEAD SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                   Rabin R, Lochrie M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-567063/53.
                                                     US2003049644-A1.
  Unidentified
                                                                                                                                                                                                            10-JUN-1991;
                                                                                                                                                                                                                                    06-JUN-1995;
                                                                                                      13-MAR-2003
                                                                                                                                                                                                                                                                                       9-JUL-1999
à
                                                                                                                                                                                                                                                    This invention describes a novel composition, and active agency, composition describes and according to reducing adenosine (short) levels of adenosine (A) or (A) receptors, cauticating adenosine sensitivity, levels of adenosine (A) or (A) receptors, cauticating adenosine sensitivity, levels of adenosine (A) or (A) receptors, curfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating (C) expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA.

CC device, in separate containers, (b) the oligonucleotides, (c) adelivery in the invention has antiallergic, antiinflammatory, antiasthmatic, of treating a respiratory, lung or malignant disease. The administered composition compasition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The composition, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vascoonstriction, distress syndrome, pain, cystic fibrosis, allergic thinitis, pulmonary charactery pain, cystic fibrosis, allergic thinitis, pulmonary characterion rejection, pulmonary infections, brain the breakdown of thy mand present in the target RNA serves to prevent the breakdown of the pain the products that free adenosine into products that free adenosine into transpersement of the prisonment and thereby the prison products that free adenosine into product that free adenosine or the prisonment and thereby.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lung, brain, heart, kidney, etc, tissue environment and thereby, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GGGCGGGGGAGAGAGGAGGGCGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GNGGGGGCNGCNGTTGGGCCCCNNNGGCCCTCTCGTTCNCCTTCTGGCNGTTGCNT 60
                                                                                                                                                                                                                                       invention describes a novel composition (a) a first active agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                              oligonucleotide containing less percentage of adenosine, targeted t
nucleic acids associated with lung airway or lung dysfunction, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
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                                                        Pharmaceutical composition for treating asthma, has antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19.6; DB 11; Length 86; Pred. No. 5.5e+03; 7; Mismatches 36; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 86 BP; 0 A; 26 C; 26 G; 19 T; 0 U; 15 Other;
                                                                                                                                                                                       Claim 15; SEQ ID NO 10602; 763pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGF aptamers-associated RNA sequence #99
     WPI; 2003-093058/08
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The invention relates to a purified and isolated non-naturally occurring uncleic acid ligand (an RNA aptamer) to hepatocyte growth factor/scatter factor (HGF) or the HGF receptor, c-met. The ligand comprises a sequence selected from 148 fully defined sequences of 17-101 bp given in the selected from 148 fully defined sequences of 17-101 bp given in the genetication. Also included are a method of treating a tumour by administering the aptamer, a method for treating a tumour by individual, a method for inhibiting angiogenesis by administering the aptamer centical excipient), a method for treating the GC in which elevated HGF is a causative factor (by administering a disease comprising administering a mucleic acid ligand to HGF) and a method for inhibiting tumour development acid ligand to HGF) and a mucleic acid ligand to vascular endothelial factor (VGGF) and/or with a nucleic acid ligands to a tleast 2 receptors of growth factors and to relators, nucleic acid ligands to at least 2 receptors of growth factors in uncleic acid ligands to a least 2 receptors of growth factors in combination with nucleic acid ligands to one or more growth factors in uncleic acid ligands to one or more growth factors in uncleic acid ligands to do one or more growth factors or aptamers comprise 2 ** F(2 ** F(10vro)) modified tibonucleic acids The combination are useful as diagnostic and therapeutic agents for hypertension, arteriosclerosis, myocardial infarction and rheumatoid are useful for inhibiting tumourispensels by inhibiting containing modified information. Nucleic acid ligands to their are useful for inhibiting tumourispensels by inhibiting and and sequences of any or erability or inproved delivery or interaction are useful for inhibiting tumourispensels by inhibiting and adjagnostic and individual are improved in vivo grability or improved delivery or interaction are useful for inhibiting tumourispensels by inhibiting tumourispensels by inhibiting tumourispensels by inhibiting tumourispensels or interaction are useful for inh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40N) surrounded by a constant region. The present sequence is an RNA sequence included in the sequence listing but not mentioned anywhere else
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.6%; Score 19.4; DB 9; Length 97; 31.1%; Pred. No. 6.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 97 BP; 42 A; 18 C; 27 G; 0 T; 7 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 31.19
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 C 79
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30 C 30

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antiasthmatic, cerebroprotective, anti-HIV, virucide; analytical chemistry; in vivo imaging; blosensor; complex matrix; affinity probe capillary electrophoresis; APCE; ELISA; fibre-optic microarray biosensor; histological marker;

tumour microvessel; anthrax spore; cocaine; ds

WO2003102212-A2

11-DEC-2003

Unidentified.

Synthetic.

CB-SELEX; capillary electrophoresis; ligand-enriched mixture;

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. S' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                        Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 14603; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 51 BP; 5 A; 23 C; 19 G; 4 T; 0 U; 0 Other;
                                                                                                                                                    Human secreted protein 5' EST, SEQ ID NO: 14603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression and secretion vectors
                                      BP.
                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2000; 2000EP-00200610.
                                                                                                                                                                                                                                                                                                                                                                                                         99US-0122487P.
                                  AAC10528 standard; cDNA; 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEST ) GENSET
                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                      EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-1999;
                                                                                                              06-OCT-2000
                                                                                                                                                                                                                                                                                                                             06-SEP-2000,
                                                                        AAC10528;
RESULT 11
                    AAC10528/
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Identifying nucleic acid ligand of target molecule from mixture comprising single stranded nucleic acids having region of randomized sequence by contacting mixture with target molecule, amplifying affinity

31-MAY-2002; 2002US-0384709P. 15-MAY-2003; 2003US-0470750P. 29-MAY-2003; 2003WO-US016796.

Bowser MT, Mendonsa SD; MINU ) UNIV MINNESOTA.

WPI; 2004-043125/04

nucleic acids.

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This invention relates to a novel method (CE-SELEX, Capillary
CE Electrophoresis-Systematic Evolution of Ligands by Exponential
CC entichment) of identifying nucleic acid ligands of a target molecule from
a candidate mixture comprised of single stranded nucleic acids each
having a region of randomised sequence by contacting the mixture with the
CC target molecule, where nucleic acids having affinity to the target
collecule are partitioned from the mixture by capillary electrophoresis,
amplifying increased affinity nucleic acids to yield a ligand-enriched
compounds with an antiasthmatic, cerebroprotective, anti-HIV or
compounds with an antiasthmatic, cerebroprotective, anti-HIV or
cof compounds with an antiasthmatic, cerebroprotective, anti-HIV or
cof compounds with an antiasthmatic, areafolder mixture comprised of single
stranded nucleic acids each having a region of randomised sequence.
CC Aptamers identified by the method are useful as a tool in analytical
cof common and acids each having a region of randomised sequence.
Aptamers identified by the method are useful as a tool in analytical
cof common and acids each having a region of randomised and health
cresearch. Improved aptamers are useful in developing diagnostic assays,
cof nemistry useful in wide range of diagnostic assays and as diagnostic markers in medical analysis, in vivo imaging
and biosensors. The aptamers are useful in developing diagnostic assays,
cof recample as diagnostic markers in medical analysis, in vivo imaging
cof present in complex matrices. The aptamers are used to develop high
cof compounts transformed endothelial calls may be selected for using fibre-optic microarray biosensors. Aptamers may be
cof against transformed endothelial calls may be selected for using fibre-optic microarray biosensors. Aptamers may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         histological markers to identify tumour microvessels. Aptamers may be developed for use in other aptamer-based assays, such as assays for analytes ranging from anthrax spores to cocaine. Aptamers having improved quality, improved binding efficiency and selectivity can be identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 GCGGGGGGGGGGGGCGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GCAGCACAGAGGTCAGATGTTGTGTACCGTTATTTGTGCCTCAGCATCCCCGTGGCTAAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the method of the invention. The present sequence is that of an aptamer DNA sequence which was identified using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 80 BP; 17 A; 21 C; 21 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 6; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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88XCCCCCCCCCCCCCCCCCCCCCCCCX
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Gaps ö

Query Match 24.3%; Score 19.2; DB 3; Length 51; Best Local Similarity 60.0%; Pred. No. 6.9è+03; Matches 24; Conservative 3; Mismatches 13; Indels

1 GGAGGGCGGGGGAGAGGAGGGCGCCCCUUAAUU 40

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47 GGGCGGCGGGCGCAGCGGCTCAGGCCCCTGCAGT

ADM79864 standard; DNA; 80

RESULT 12 ADM79864

ADM79864;

03-JUN-2004 (first entry)

2×2×2×2×

DNA ligand identification-related aptamer DNA sequence SeqID6.

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Gaps

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62 99

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ABX51458

RESULT 13 ABX51458

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New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel genes (AAH68727-AAH73383) associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                        Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 4; Length 65; Pred. No. 8.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Indels
                                                                        Indela
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                                                                                                                                                        40 uguacuncegecucenatueucucuccuuteeccaccucc 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 TTTTCTTCGTCNTCGAANANTCTCTTCCTTCGCTNNCGCC
                                                                                                                           31 ccccumaaunguacuncegecuceuaungucucuccunuc
                        24.3%; Score 19.2; DB 8; 37.5%; Pred. No. 7.7e+03; ive 12; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cervical cancer marker nucleic acid 271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 150; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-1999; 99US-0169681P.
21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189315P.
12-MAY-2000; 2000US-0203791P.
09-UJN-2000; 2000US-0210600P.
21-JUL-2000; 2000US-021014P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-2000; 2000WO-US03312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
24.1%;
Best Local Similarity 37.5%;
Matches 15; Conservative 10
AAH68997 standard; cDNA; 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADX69632 standard, DNA; 97
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-375006/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200142467-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADX69632;
                                                                                                                                                                                                                                                                                                                                                               AAH68997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful
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                                                                                                                                                                                                                                                            RESULT 14
AAH68997/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADX69632
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AC ADX6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 5912 nucleotide sequences, appearing as BAX50072-ABX593, or complements of them. Also included are if it aransformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3, non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and cl polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and cl the 5912 nucleic acid sequences or its complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) where the sevel or pattern of the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid permits the detection of the molecule; and (c) detecting the level or pattern of the complementary nucleic acid sequences or its complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is used for the detection of the complementary nucleic acid is used for level or pattern of the molecule. The LMFD nucleic acid is used for the or pattern of the molecule. The LMFD nucleic acid is used for the sequence mapping, gene identification and analysis, cattle for genome mapping, gene identification and analysis, cattle breading, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 5912 bovine LMFD EST (expressed sequence was not shown in the specification but was obtained in the best of the construction of the construction but was obtained in the best of the construction of the construction but was obtained in the best of the construction of the constr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
of constructs
                                                                                                                                                                                                                                                                                                                                                                                 Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                            Bovine EST associated with lactation/muscle/fat deposition #1387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Purified nucleic acid molecules, useful for genome mapping, identification and analysis, cattle breeding or preparation for cattle gene expression and genetically improved cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 87 BP; 28 A; 28 C; 3 G; 28 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      segdata.uspto.gov/seguence.html?DocID=20020137160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; SEQ ID NO 1387; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tao N,
                                                                                                                                                                                      ABX51458 Btandard; cDNA; 87 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-OCT-2001; 2001US-00983965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0113678P.
                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mathialagan N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BYATT J C.
MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TAON/) TAO N.
(WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-102386/09
                                        |: :
CTAT 65
        COUTT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002137160-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-DEC-1998;
15-DEC-1999;
                                                                                                                                                                                                                                                                                         25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos Taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Byatt JC,
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BYAT/) (MATH/)

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Gape ö

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The invention relates to an anti-HM1.24 (I) antibody which has a modified sugar chain. Also included are an antibody composition, containing (I) in which the sugar chain ides not contain fucose and the relative ratio of the sugar chain is 30% or more and producing the antibody. The modified antibody is produced by culturing a host cell in which the ability of the cell to add fucose in the sugar chain of the antibody, is deleted, and in which the nucleic acid encoding the anti-HM1.24 antibody is introduced, by culturing a host cell in which nucleic acid encoding N-acetyl

Comparison of the antibody is introduced, and in which the nucleic acid encoding N-acetyl

Comparison of the antibody is introduced, and in which the nucleic acid encoding N-acetyl

Comparison of the subsection of the antibody is introduced, and in the cultured solution. The antibody does not contain alpha-1, 6 core fucose and/or has a sugar chain having a bisecting N-acetylglucosamine cluck tumor and is useful as a therapeutic agent for treating myeloma such as multiple myeloma. The antibody-dependent cellular cytotoxicity (ADCC) of the antibody) is enhanced by the sugar chain modification. The present comparison the present contain alpha-1, 6 core the antibody) is enhanced by the sugar chain modification. The present contain alpha-1, 6 core the antibody is enhanced by the sugar chain modification. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-HM1.24 antibody useful for diagnosis of a tumor and useful as a therapeutic agent for treating myeloma, comprises a modified sugar chain.
                                                                                                        Antibody engineering; radioimmunotherapy;
antibody-dependent cellular toxicity;
n-cetyl glucosaminyl transferase III; ss; PCR; primer; Cytostatic;
Immunotherapy; tumor; neoplasm; multiple myeloma; hematological disease;
immune disorder.
                                                                  Human GnTIII mutagenic forward PCR primer 1-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugo I, Sugimoto M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; SEQ ID NO 2; 58pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                              11-AUG-2004; 2004WO-JP011812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-AUG-2003; 2003JP-00207165
                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsuchiya M, Iijima S,
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                                                                                                                                                                                                                                                 Homo sapiens.
Synthetic.
                     05-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                 17-FEB-2005
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Sequence 97 BP; 15 A; 34 C; 16 G; 32 T; 0 U; 0 Other;

Query Match
24.1%; Score 19; DB 14; Length 97;

Best Local Similarity 38.8%; Pred. No. 9.2e+03;

Matches 26; Conservative 11; Mismatches '30; Indels 0; Gaps

72 CCACCUC 78

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8 8

63 GCACTTC 69

Search completed: October 16, 2006, 14:32:17 Job time : 305 secs

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CW236987 104 693 1
H25883 Y49910.81
CW067844 104 315.1
AV957037 AV957037—
CO167237 ED15.68—C
AI360975 GY02F12.x
AU105862 AU105862
CW022621 104 162 1
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AI539851 tp65f05.x
DU106469 JBNY028G0
DU106469 JBNY028G0
DX106469 JBNY028G0
DX106469 JBNY028G0
BX289701 Arabidops
CR587313 AZ605020 1M0426G10
AZ770277 1M0571E16
AA691640 v813a07.r
BM157107 fv44604.y
AK192966 MUS mUSCU
AA65933 INISC GF05
DY248960 CSTFBID04
CD945332 RDXZ GGD
BJ029975 GC10902.
                                                                                                                                                                                                                                                                                                                                                                                                                          DX728792 XGC-tadpole Xenopus tropicalis cDNA clone TTpA036j08 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contract: Croning MDR
Sanger Institute
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TTPA036j08.plkSP6
Sequencing primer: $P6
Sequencing primer: $P6
Sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
cDNA was oligo dT primed from sug of poly A+ RNA from tadpole
embryos. ECCRI-NotI cut CDNA was then ligated into pCS107 with
ECORI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: ECORI; Site 2: NotI
HOST: ESCherichia coli DH10B.
Location/Qualifiers
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1 (bases 1 to 76)
1 (bases 1 to 76)
2 (Coning, M.D. R., Ashuret, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                     CW067844

AV957037

A0105862

A0105862

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A0105861

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A0106469

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 mRNA sequence.
BX728792
  18.8
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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BX728792
LOCUS
DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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 BX728792 BX728792
AA414137 vd07h01.8
AI583881 ttr0bb4.x
AI585698 gw89£06.x
BQ382202 kk43e03.y
BF447704 us40a01.x
AI616438 zehn0074.
CCL83143 XE629 Bay
H55638 CHR220577 C
CT351516 Sus scrof
CW115559 104 490.1
CW115559 104 490.1
CW125159 CRC666 TI
CW20424 GC0666 TI
DT21192 PCRS60390
AJ549396 AJ649396
AA437593 vd05£03.8
                                                                                    ; Search time 4326 Seconds (without alignments) 1021.181 Million cell updates/sec
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                                                                                                                                                                1 ggaggggggggagagacga........ncucuccuuucgccaccucc 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
             GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                          853524
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                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                             nucleic search, using sw model
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AA414137
AIS3381
AI269698
BR28222
BR147204
AIG6438
CC183143
HS5638
CW115559
CW11559
CW15559
CW15559
AM437593
AZ769498
CR076775
                                                                                       October 16, 2006, 14:23:36
                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                 US-10-604-726A-5135
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Match Length DB
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Maximum DB seq length: 100
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                                                             OM nucleic -
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Database :

Result No.

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Sequence:

Run on:

Searched:

/clone="TTPA036j08"
/dev stage="tadpo16 (stage 35-40)"
/dev stage="tadpo1 (stage 35-40)"
/lab\_host="E. col1 DH108"
/clone lib="XGC+tadpo1e"
/note="Vector: pCS107; Site 1: BcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from tadpole

AZ769498 1M0570K16 CR076775 Reverse B DN441479 LIB5338-1

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Momindae; Momo.

1 (Dases 1 to 91)

Rational Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Theory Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-r@mail.nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A1269688 91 bp mRNA linear EST 17-NOV-1998 gw89f06.x1 NCI CGAP Brn35 Homo sapiens cDNA clone IMAGE:1998275 3' 81milar to TR:Q14934 NF-AT3. ;, mRNA sequence. A1269598.1 GI:3888865
                                                                AI583881 107 CGAP HSC3 Homo applens CDNA clone IRAGE:2246095 3' TCTD0b04.x1 NCI CGAP HSC3 Homo applens CDNA clone IRAGE:2246095 3' similar to TR:063624 063624 CTD-BINDING SR-LIKE PROTEIN RA1. ;contains element TAR1 TAR1 repetitive element ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib.mrc CGAP HSC3"
/note=Torgan bone marrow, Vector: pAMP1; mRNA made from /note=Torgan bone marrow, Vector: pAMP1; mRNA made from lymphoid tissue, cDNA made by oligo-dr priming.
Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:2246095"
/tissue_type="CD34+, T negative, patient with chronic myelogenous leukemia"
/lab_host="MH106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 gecegegagagaceaececucuesceccumaauuguacuucesecuceuauugucucu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 26.8%; Score 21.2; DB 1; Length 91; Similarity 33.3%; Pred. No. 2.3e+04; 25; Conservative 16; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trace considered overall poor quality
Seg primer: -400P from Gibco
High quality sequence scop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                 AI583881.1 GI:4569778
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Homo sapiens
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                     RESULT 3
AI583881
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1. (bases 1 to 84)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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/note="Organ: embryo; Vector; pBluescribe (modified);
Site_1: Mlu!; Site_2: Sall; Cloned unidirectionally from
RNA prepared from 13,500 2-cell stage embryos. Primer:
Sall(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTTT-3'.
pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."
embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:476265
Seg primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                             Length 76;
                                                                                                                                        9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 AUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUCGCCACCUCC 79
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                                                                                           27.3%; Score 21.6; DB 4;
ilarity 41.7%; Pred. No. 1.6e+04;
Conservative 12; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FI.
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/strain="C57BL/6J x DBA/2J
/db_xref="taxon:10090"
/clone="IMAGE:791857"
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/dev_stage="2-cell"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                        AA414137.1 GI:2074294
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Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter at Washington University, St. Louis. The CDNA was made by
McCarter at Washington University, St. Louis. The CDNA was made by
using Dynabead oligo-dr priming (Dynal). PCR based library using a
modified protocol from the SWART PCR cDNA Synthesis Kit from
Clontech. Directionally cloned into the UGG sites of pAMP1.
Dissected nematode tissues were provided by Dr. Alan Scott
(ascott@jhsph.edu) of the School of Public Hygene and Public Health
at John Hopkins University in Baltimore, MD.
Seq primer: T7 from Gibco
High quality sequence stop: 99.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pAMP1 (Gibco); Site_1: Not1; Site_2: Sal1; The library was constructed by Brandi chiapelli and Dr. James McGarter at Washington University, St. Louis. The CDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR CDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1, Dissected nematode tissues were provided by Dr. Alan Scott (ascott@lisph.edu) of the School of Public Hygene and Public Health at John Hopkins University in Baltimore, MD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF147704 150 area NMEBA branchial arch Mus musculus cDNA clone IMAGE:3169512 3' Similar to TR:Q15022 Q15022 ORF ;, mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Intestine"
/dev stage="Adult"
/dab_hose="BH10B"
/clone_lib="Ascaris suum male gut pAMP1 v2 Chiapelli
                                                    The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TEL: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.1%; Score 20.6; DB 3; Length 100; 42.4%; Pred. No. 3.7e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Ascaris suum"
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Unpublished (1997)
Other ESTs: us40a01.y1
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:6253"
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BF147704/c
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                                 COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbe-remail.nib.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A. (G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/lmage/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCICGAP_Brn35"
/note=Torgan: brain; Vector: pCWV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.33 kb. Tumor types include:
meningioma, oligodendroglioma, astrocytoma (grade II),
medulloblastcma, astrocytoma (grade IV). Life Technologies
catalog #: 11544-012"
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McCarter, J. Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wylie, T., Dante, M., Marra, M., Hillier, L., Rucaba, T., Theising, B.,
Wylie, T., Dante, M., Marra, M., Hillier, L., Rucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 91)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI/ONINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
OALIONAL Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 GCUCUGGCCCCUUDAUUGUACUUCGGCCUCGUAUUGUCUCCUCCUUUCGCCACCUCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="tumor, 5 pooled (see description)" /lab_host="DH108"
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Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;
Ascaridoidea; Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.3%; Score 20.8; DB 1; Length 91; 33.9%; Pred. No. 3.1e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trace considered overall poor quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:1998275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seg primer: -400r ...... High quality sequence stop: 1.
Location/Qualifiers
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/db_xref="taxon:9606"
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                                                             Homo sapiens
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Best Local Similarity
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AUTHORS
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BQ382202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zehn0074.seq.F Zebrafish Embryonic Heart CDNA Library Danio rerio Alise 5, mRNA sequence.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CSAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LML at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="embryo, 10.5 dpc"
/lab_host="DH10B (phage resistant)"
/lab_host="DH10B (phage resistant)"
/lone=libh="Soares" NPBA = Dranchial arch"
/note="Vector: PT773D-Pac1; Site 1: Not1; Site 2: EcoRI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liew,C.C.
Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3']; double-stranded cDNA was ligated to Eco RI adaptors Pharmacia), digested with Not I and cloned into the Not I and Eco RI stres of the modified pr773 vector. Library constructed and normalized by Bento Soares and M.Fatima
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mably, J.D., Dempsey, A.A., Hwang, D.M., Fishman, M.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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BACKWARD: 5' CCAGTGAATTATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAAATTAACCTCACTAAAGGG 3'.
Location/Qualifiers
                                                                                                                                                                     Trace considered overall poor quality Possible reversed clone: polyr not found High quality sequence stop: 1.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="branchial arches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brigham and Women's Hospital
Harvard Medical School
Francis St. Boston, MA 02115, USA
Tel: 6177328915
                                                                                                                                                                                                                                                            1. .85
/organism="Mus musculus"
/organism="Mus musculus"
/ol_type="mxnn"
/db xref="taxon:10090"
/clone="IMAGE:3169512"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cliew@rics.bwh.harvard.edu
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XE629 BayGenomics Gene Trap Library pGT1Lxf Mus musculus CDNA, mRNA
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CELL_LINE&KEY=XE629
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                                                                    /dev stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XL1-Blue mrF" "
/clone lib="zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart, Vector: Lambda ZAP Express; Site 2:
ECORI; Site 2: XhoI; mRNA was purified from embryonic zebrafish hearts (3 day post-fertilization). cDNA was adaptors were ligated, followed by digestion with XhoI, for directional cloning into pre-digested lambda ZAP Express vector. "
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
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Bay Area Punctional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
equence tag generated by 5' RACE of total RNA from gene trapectl line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 81;
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/clone lib="BayGenomics Gene Trap
/note="Vector: pGTlLxf"
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    .81
    /organism="Mus musculus"
/mol_type="mRNA"
    /strain="129 ola"

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mol_type="mRNA"
db_xref="taxon:7955"
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Unpublished (2001)
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CC183143.1 GI:30427043
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Class: Gene Trap.
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Sorghum bicolor (sorghum)
Sorghum bicolor
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CW115558.1 GI:54808105
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/mol_type="mRNA"
/do_tref="taxon:9606"
/dlone="122_78;"
/lab_host="\overline{E}. coli DH5a"
/clone="122_78;"
/lab_host="\overline{E}. coli DH5a"
/clone="loctromosome 22 exon"
/note="vector: pBluescriptIIKS+; Site_1: Sal I; Site_2: Anote="vector: pBluescriptIIKS+; Site_1: Sal I; Site_2: Anote="vector: pBluescriptIIKS+; Site_1: Sal I; Site_2: Chromosome 22 specific cosmids using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88:4005-4009, 1991). Amplified exons were digested with Sal I and Bal II and subsequently cloned into pBluescriptIIKS+ at the Sal I and Bam HI sites."
                                                                                                                                                                                                                                                                                 Hominidae, Homo.

1 (bases 1 to 88)

Trofatter, J.A., Long, K.R., Murrell, J.R., Stotler, C.J., Gusella, J.F.
and Buckler, A.J.

An expression-independent catalog of genes from human chromosome 22
Genome Res. 5 (3), 214-224 (1995)
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Humphray, S. J., Plumb, R.W. and Durham, J.L.
Direct Submission

Direct Submission

Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
                                                                              H55638

88 bp mRNA linear EST 07-DEC-1995
CHR220577 Chromosome 22 exon Homo sapiens cDNA clone C22_783 5',
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Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Sus scrofa genomic clone CH242-438014, genomic survey sequence.
CT351516.1 GI:79928188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular Neurogenetics Unit
Massachusetts General Hospital
Building 149, 13th St., Charlestown MA 02129
Fax: 6177249616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: buckler@helix.mgh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                             H55638.1 GI:1108504
                                                                                                                                                                                                  Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Buckler AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . .88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T3.
                                                                                                                        mRNA sequence.
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CT351516/c
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                                     RESULT 9
                                                      155638/c
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Inote="Organ: leaf, Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electropozated into E. coli cells. This is a methylation filtered library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CW115558 110.6626 116 34591 001 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11106626, genomic survey
This sequence was generated from the T7 end of BAC 438014. 438014 is part of the CH012-242 BAC Library created by P. de Jong. Further details: http://www.sanger.ac.uk/Projects/S_scrofa/. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
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/organism="Sorghum bicolor"
/organism="Sorghum bicolor"
/mol type="genomic DNA"
/culfivar="ATx623"
/db_xref="taxon:4558"
/clone="1110626"
/clone_lib="Sorghum methylation filtered library (LibID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 83)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 CCUDAAUUGUACUUCGGGCUCGUAUUGUCUCCUCCUUUCGCCACCUCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 490 row: o column: 02
Seq primer: T3 Reverse
Class: methylation filtered
High quality sequence stop: 83.
                                                                                                                               1. 78
/organism="Sus scrofa"
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/db_xref="taxon:9823"
/clone="CH242-438014"
/tissue_type="White blood cells"
/note="Yector pTARBAC1.3_BamHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.1%; Score 19.8; DB 14; Best Local Similarity 38.3%; Pred. No. 6.8e+04; Matches 18; Conservative 12; Mismatches 17;
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LOCUS DEFINITION

RESULT 12

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CW115559

ACCESSION VERSION KEYWORDS

REFERENCE AUTHORS

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CW020424 11GEM gene trap library Mus musculus cDNA clone A011.G4,
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PCRS50390_2 Hematopoietic stem cells Mus musculus CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                              Cobellis,G., Nicolaus,G., Iovino,M., Romito,A., Marra,E.,
Cobellis,G., Nicolaus,G., Iovino,M., Di Giorgio,F.P., Iovino,N., Zollo,M.,
Ballabio,A. and Cortese,R.
Tagging genes with cassette-exchange sites
Nucleic_Acids Res. 33 (4), e44 (2005)
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Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGAGGGGGGGGAGAGAGGGGCCUCUGGCCCCUUAAUUGUACUUCGGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 24.8%; Score 19.6; DB 13; Length 71; Similarity 52.0%; Pred. No. 7.8e+04; 26; Conservative 5; Mismatches 19; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="TIGEM gene trap library"
/note="Vector: pFLIP1"
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/cell_type="Embryonic stem cell"
/cell_line="E14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
/clone="A011.G4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                               mRNA sequence.
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    75 TCT 77
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Best Local Si
Matches 26;
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SOURCE
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CW020424
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Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Sorghum methylation filtered library (LibID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGGCGGGGGAGAGAGCGGCCCCCUUAAUUGUACUUCGGGCUCGUAUUGUC 61
                                                                                                                     67 GAAGACGGCCTCATCGGGGCCAACCTGGACCTTAAATAGGAAGACGCGCTCGTCAGGTT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 83)
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
McMenamy, J., Smith, M., Holeman, H., Roe, B.A, Wiley, G., Korf, I.F.,
Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and
Martienssen, R.A.
                                                                                              2 GAGGCCGGGGGAGAGACGAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUC
                                                   Gape
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       DB 13; Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sorghum genome sequencing by methylation filtration PLoS Biol. 3 (1), e13 (2005)
  Score 19.8; DB 13; Length
Pred. No. 6.8e+04;
8; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbdell@coriongenomics.com
Plate: 490 row: o column: 02
Seq primer: SWfor Porward
Class: methylation filtered
High quality sequence stop: 83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/cultivar="ATx623"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                         CW115559
CW115559.1 GI:54808106
Query Match 25.1%;
Best Local Similarity 44.4%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
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7 TCT 5
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Roslin, Midlothian, EH25 9PS, UNITED KINGDOM Single pass sequencing. Bases called and trimmed with phred vo.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(KS) R. Sitel: ECORI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pooled ovaries. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK, EH25 9PS, www.ark-genomics.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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/mol type="mmkh"
/db xref="taxon:9823"
/clone="color: youry"
/clone lib="CSEQRAN19"
/note="yourcr: pBlueScript11(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing; Normalised library
constructed from pooled ovaries"
Diversification of Stem Cell Molecular Repertoire by Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GCGCUCUGGCCCCUUAAUUGUACUUCGGCUCGUAUUGUCUCCCUUUCGCCACCUC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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/tisuse_type="Hematopoietic stem cells"
/clone_lib="Hematopoietic stem cells"
/clone_lib="Hematopoietic stem cells"
/clone_lib="Hematopoietic stem cells"
/note="ColMA library was made from FACS-purified hematopoietic stem cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                      Contact: Pritsker M
Lab of Ihor Lemischka, Department of Molecular Biology
Princeton University
Princeton 308544, USA
Tel: 609 258 5657
Fax: 609 258 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

24.8%; Score 19.6; DB 10; Length
Best Local Similarity 36.2%; Pred. No. 8e+04;
Matches 21; Conservative 13; Mismatches, 24; Indels
                                                 Proc. Natl. Acad. Sci. U.S.A. (2005) In press
                                                                                                                                                                                                                            Email: pritsker@molbio.princeton.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
                          Splicing
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AJ649396
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TITLE
                                                 JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
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                                                                                                                                                                                                                                                      FEATURES
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  TITLE
                                                                            COMMENT
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        Query Match
        24.8%; Score 19.6; DB 1; Length 85;

        Best Local Similarity 42.0%; Pred. No. 8e+04;

        Matches 21; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

        Qy
        16 GAGGGGGGCUGGGCCCUNANUGUCUCUC 65

        P | | | | | | | | | | | | | | | |

        Db
        8 GTGGGGAGGCCTGGCCTCCCTCCTCCTCCTCCTCTC 57
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Search completed: October 16, 2006, 16:16:48 Job time: 4331 secs

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COUNTRY: USA
US-09-543-679A-1233
                                                                                                                                                                                                                           RESULT 1
00000000
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Sequence 18431, A
Sequence 12, Appl
Sequence 12, Appl
Sequence 288, App
Sequence 288, App
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415, App
27, Appl
27, Appl
27, Appl
15806
86, Appl
86, Appl
16, Appl
16, Appl
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11, Appl
11, Appl
19, Appl
                                                         October 16, 2006, 14:28:14 ; Search time 110 Seconds (without alignments) 1343.796 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                           /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                      Description
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         5.1.9
Biocceleration Ltd
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US-09-621-976-18431
US-08-011-4723-12
US-08-110-011A-12
US-08-110-011A-12
US-08-1949-928-288
US-09-849-928-288
US-09-813-999C-14603
US-08-014-723-11
US-08-014-723-11
US-09-513-999C-14633
US-08-014-011A-11
US-09-911-927-27
US-09-911-927-27
US-09-911-927-27
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US-09-911-988-27
US-09-911-988-27
US-09-911-988-27
US-09-911-988-27
US-09-911-988-27
US-09-911-911-928-08
US-08-410-28
US-08-410-28
US-08-09-13-16
                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-488-031-16
US-08-486-569-16
                                                                                                                                                   1403666 segs, 935554401 residues
         GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         nucleic search, using sw model
                                                                                                                          IDENTITY_NUC Gapopt 10.0
                                                                                        US-10-604-726A-5135
79
                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 100
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Match
                                                                                         Title:
Perfect score:
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19.8
19.4
19.4
2.4
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                                                         Run on:
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16, Appl
16, Appl
16, Appl
16, Appl
25, Appl
68, Appl
847, App
847, App
53, Appl
53, Appl
13, Appl
13, Appl
13, Appl
                                                                                                                                                                                                                                                                                                        Sequence 13, App
Sequence 15862,
Sequence 13448,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-03-33-3-75-123, Application US/09543679A
Sequence 1233, Application US/09543679A
Patent No. 7034007
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF ATREAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
                    Sequence
Sequence
Sequence
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Sequence
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Sequence
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     Sequence
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ADDRESSE: BPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
                                                                                                                                                                                                                                                                                                    PCT-US96-06059-13
US-09-513-999C-15862
US-09-621-976-13448
US-08-482-663-16
US-08-482-663-16
US-08-475-610-16
US-08-475-610-16
PCT-US92-00277-16
PCT-US92-00277-16
US-09-873-075A-5
US-09-393-803-68
US-10-131-831-847
US-10-131-831-847
US-09-371-774-53
US-09-371-774-53
US-08-433-124A-13
US-08-433-124A-13
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FILING DATE: 1998-08-03
ATTORNEX/AGENT INFORMATION:
NAME: Amzel, Viviana
REFERATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILITHG DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: Genomic DNA SEQUENCE DESCRIPTION: SEQ ID NO: 1233:
                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1233:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 413-254-9245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 08512
COMPUTER READABLE FORM:
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APPLICANT: Doi, Takeshi
APPLICANT: Iwasaki, Akio
APPLICANT: Iwasaki, Akio
APPLICANT: Saino, Yushi
APPLICANT: Shura, Shigeru
APPLICANT: Ohkuchi, Masao
TITLE OF INVENTION: Thrombin-Binding Substance and Process
TITLE OF INVENTION: Por Preparing the Same
NUMBER OF SEQUENCES: 18
CORRESPONDENCE S: 18
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.1%; Score 19.8; DB 2; Length 6 Best Local Similarity 59.0%; Pred. No. 5.6e+02; Matches 23; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AGGCCGGGGAGAGACGAGCGGCUCUGGCCCCUUAAUUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 AGGTCGACGACGAGGCCACCAGCGCTCTGGCGACTGACTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/110,011A
PTLING DATE: 23-AUG-1993
TLING DATE: 23-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5354664man F.
REFERENCE/CONTON INFORMATION:
TELEPHONE: (703)413-2220
TELEPHONE: (703)413-2220
TELEFAX: (703)413-2220
TELEFAX: (703)413-2220
TELEFAX: CARRETERISTICS:
INFORMATION FOR SEQ ID No: 12:
LENGTH: 63 bases
                                                                                                                                                       80-071-0 CIP
                APPLICATION NUMBER: US/08/014,723
FILING DATE: 19930208
CLASSIFICATION: 435
                                                                      CLASSIFLLION:
ATTORNEY/AGENT INFORMATION:
NAME: ODION, NO. 5273962man F.
REGISTRATION NUMBER: 24,618
REFERENCE FOOKET NUMBER: 24,618
REFERENCE (703)413-3000
TELEPHONE: (703)413-220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
TYPE: NUCLEIC ACID
STRANDEDRESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-110-011A-12/c; Sequence 12, Application US/08110011A; Patent No. 5354664
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
HOLECULE TYPE: DNA (genomic)
US-08-014-723-12
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STRANDEDNESS: single
TOPOLOGY: linear
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STATE: Virginia
ZIP: 22202
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                                                                                                                                    4 GGGCGGGGGGAGACGACGCGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUC 63
                                                                                                                                                            Gaps
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APPLICANT: Iwasaki, Akio
APPLICANT: Iwasaki, Akio
APPLICANT: Saino, Yushi
APPLICANT: Kimura, Shigeru
APPLICANT: Ohkuchi, Masao
ITILE OF INVENTION: Thrombin-Binding Substance and Process
ITILE OF INVENTION: For Preparing the Same
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
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                                        25.8%; Score 20.4; DB 5; Length 86; 38.6%; Pred. No. 3.6e+02; tive 17; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 93;
                                                                                                                                                                                                                                                                                                                                                                            Sequence 18431, Application US/09621976

(GENERAL INPORMATION:
(GENERAL INFORMATION:
(APPLICANT: Johnes Mine Edwards, J.B.
(APPLICANT: Glordano, J.Y.
(TILE OF INVENTION: ESTS and Encoded Human Proteins.)
(TILE REFERENCE: GENSET.054PR2
(CURRENT APPLICATION NUMBER: US/09/621,976
(CURRENT FILING DATE: 2000-07-21
(NUMBER OF SEQ ID NOS: 19335
(SOFTWARE: Patent.pm
(SEQ ID NO 18431
(LENGTH: 93)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGGGGGAGACGAGCGCCUCUGGCCCCUUAAUU 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 25.3%; Score 20; DB 3; Cocal Similarity 63.9%; Pred. No. 5.2e+02; Pred. 23; Conservative 3; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-08-014-723-12/c
; Sequence 12, Application US/08014723
; Betent No. 5273962
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | NAME/KEY: misc_feature
| DCCATION: 63...64,83
| OTHER INFORMATION: n=a, g, c or t
| US-09-621-976-18431
                                                                                       27; Conservative
                                                                                                                                                                                                                           64 UCCUUUCGCC 73
                                                                                                                                                                                                                                                     61 CCCCBTBGTC 70
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ORGANISM: Homo sapiens
                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                US-09-621-976-18431/C
US-09-543-679A-1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                       Matches
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19 GAGGGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUCGCCACCUC
                                                 Gaps
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    Length 97;
                                                                                                                                                                                                                                                                                                                                                             Sequence 288, Application US/09849928
Patent No. 6544959
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
APPLICANT: PARMA, TOHICH APPINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: TO LECTINS
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: All C'8 are 2'-NH2 cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB COMPUTER: IBM pc compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SEQUENCE DESCRIPTION: All U's are 2'-NH2 uracil; SEQUENCE DESCRIPTION: SEQ ID NO: 288: US-09-849-928-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
  24.6%; Score 19.4; DB 3; ilarity 31.1%; Pred. No. 8.9e+02; Conservative 16; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,215
REPERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/849,928
FILING DATE: 04-May-2001
CLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/952,793
FILING DATE: «Unknown-
FILING DATE: «Unknown-
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/477,829
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 288: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Barry J. Swanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Englewood
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                           Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                         US-09-849-928-288/c
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       Query Match
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                                                                                                   Length 63;
                                                                                              Query Match 25.1%; Score 19.8; DB 2; Length 6. Best Local Similarity 59.0%; Pred. No. 5.6e+02; Matches 23; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                               % Sequence 288, Application US/08952793
; Sequence 288, Application US/08952793
; Patent No. 6280332
; Patent No. 6280323
; Patent LINCOMATION:
    APPLICANT: PARMA, et al.
    TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS; TITLE OF INVENTION: TO LECTINS
; VUMBER OF SEQUENCES: 390
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Swanson & Brateshun, L.L.C.
    ADDRESSEE: Swanson & Brateshun, L.L.C.
                                                                                                                                                                                                41
                                                                                                                                                                                                                      40 AGGTCGACGACGACGACCACCACTGACTCG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         All C's are 2'-NH2 cytosine
                                                                                                                                                                                                ; OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-952-793-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTONNEY/AGENT INFORMATION:
NAME: BARTY J. SWAIBON:
REGISTRATION NUMBER: 33,215
REGISTRATION NUMBER: 33,215
REGISTRATION NUMBER: 33,215
REGISTRATION NUMBER: 33,215
REGISTRATION NUMBER: 08/477,829
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDERfect 6.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,793
    Other nucleic acid;
DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 288:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 97 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Englewood
Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
; MOLECULE TYPE:
; DESCRIPTION:
US-08-110-011A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CC
COUNTRY:
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Gaps

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US-09-13-999C-14603/C

i Sequence 14603, Application US/09513999C

j Batent No. 678361

i GENERAL INFORMATION:

i APPLICANT: Dunas Milne Edwards, J.B.

i APPLICANT: Duclart, A.

i APPLICANT: Glordano, J.Y.

i TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PATENTE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 1999-02-24

PRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: PATENT.

EMOTTH: 51

LENOTH: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Doi, Takeshi
APPLICANT: Iwasaki, Akio
APPLICANT: Saino, Yushi
APPLICANT: Kimura, Shigeru
APPLICANT: Kimura, Shigeru
APPLICANT: Ohkuchi, Masao
TITLE OF INVENTION: Thrombin-Binding Substance and Process
TITLE OF INVENTION: For Preparing the Same
CORRESPONDENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.3%; Score 19.2; DB 3; Length 51; 60.0%; Pred. No. 8.9e+02; tive 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGAGGCCGGGGAGACGACGGCCCCCCUDAAUU 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,723
FILING DATE: 19930208
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5273962man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08014723 Patent No. 5273962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0%
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Arlington
STATE: Virginia
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
79 C 79
                                               30 C 30
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                                19 GAGCGCCUUUGGCCCCUUAAUUGUACUUCGGCUCGUAUUGUCUCUCCUUUCGCCACCUC 78
  19 GAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUCGCCACCUC 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09455A
FILING DATE: 05 JUNE 1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    All C's are 2'-NH2 cytosine
                                                                                                                                                                                                                             PCT-US96-09455A-288/C
Sequence 288, Application PC/TUS9609455A
Sequence 288, Application PC/TUS9609455A
SEMERAL INFORMATION:
TITLE OF INVENTION: LIGANDS TO LECTINS
TITLE OF INVENTION: LIGANDS TO LECTINS
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: SWANBON & Bratechun, L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: All U's are 2'-NH2 uracil
PCT-US96-09455A-288
                                                                                                                                                                                                                                                                                                                                                                     STREET: 8Wanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Brailewood
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION DATA:

RPEIOR APPLICATION DATA:

APPLICATION NUMBER: 08/479,724

FILING DATE: 07-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/472,256

FILING DATE: 07-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/472,255

FILING DATE: 07-JUNE-1995

PRIOR APPLICATION NUMBER: 08/477,829

PILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: 33,215

REFERENCE/DOCKET NUMBER: 33,215

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: 33,215

REFERENCE/DOCKET NUMBER: 33,215

RELEPAN: (303) 793-3333

TELEBHONE: (303) 793-3433

INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs

TYPE: nucleic acid

STRANDEDESS: alingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: RNA
                                                                                                79 C 79
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30 AGGTCGACGACGAGGCCAGCGGCTCTGGCGACTGA 64
                                                                              US-09-367-791A-19; Sequence 19, Application US/09367791A; Patent No. 6573071; Patent No. 6573071; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 44.7<sup>3</sup>
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-444-818-753/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08110011A

Patent No. 5354664

GENERAL INFORMATION:
APPLICANT: Doi, Takeshi
APPLICANT: Saino, Yushi
APPLICANT: Masaci, Akio
APPLICANT: Ghkuchi, Masao
TITLE OF INVENTION: Thrombin-Binding Substance and Process
TITLE OF INVENTION: Thrombin-Binding Substance
CORRESPONDENCE ADDRESS:
ADDRESSEE: DOLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                       Length 65;
                                                                                                                                                                                                                                Query Match 24.1%; Score 19; DB 2; Length 65; Best Local Similarity 62.9%; Pred. No. 1.1e+03; Matches 22; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUDRESSEE: COLUM, SPIVAK, MCCLELLAND, MAIER & NEUS STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Allington STATE: Virginia ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/08/110,011A
FILING DATE: 23.AUG-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                     3 AGGCGGGGGAGACGAGCGGCUCUGGCCCCUUA 37
                                                                                                                                                                                                                                                                                                                                                                30 AGGICGACGACGAGGCCAGCGGCICTGGCGACTGA 64
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NAME: Oblon, No. 5354664man F.
REGISTRATHON NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-073-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-2220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other nucleic acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESCRIPTION: DNA (synthetic)
                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-014-723-11
               TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 65 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.37
Best Local Similarity 62.37
Conservative
(703)413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 65 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-110-011A-11
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TELEFAX:
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3 AGGCCGCGCGCACACCACCGCCCCCUVA 37

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APPLICANT: Himmelspach, Michele
Schlokat, Uwe
Schlokat, Uwe
Dorner, Friedrich
Fisch, Andreas
Eibl, Johann
TITLE OF INVENTION: Pactor X Analogues With
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.8%; Score 18.8; DB 3; Length 39; 44.7%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 753, Application US/08444818
Patent No. 6150087
BARBAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 CCUUDANTUGUACUTCGGGCUCGUAUTGUCUCCUCCUTUC 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/367,791A
FILING DATE: 12-No. 6573071-1999
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-367-791A-19
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Query Match
Best Local Similarity
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67 TC 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GCCGCGCGAGAGCGACCGCCCCCCTAAUUGUACUCCGGCCCCCUAUU 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.8%; Score 18.8; DB 3; Length 54; 48.1%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 415, Application US/08687421
; Patent No. 6177557
; GENERAL INPORMATION:
    APPLICANT: Janjic, Nebojsa
    APPLICANT: Tasset, Dianne
    TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
    TITLE OF INVENTION: FIRROBLAST GROWTH FACTOR AND
    TITLE OF INVENTION: TRROMBIN
    NUMBER OF SEQUENCES: 445
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.0 CURRENT APPLICATION DATA:
FILLING DATE: 08-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                             COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: B400 E. Prentice Avenue, Suite 200 CITY: Englewood STATE: Colorado COUNTY: USA
ZIP: B0111
COMPUTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIERCATION: 424
CLASSIERCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: HARBIT INFORMATION:
REGISTATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEPHONE: (50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer JHC 13"
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Conservative
                                                                   STREET: 4560 Hort
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 26; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-08-687-421-415
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## APPLICATION WNBER: 08/195,005
## PRIOR APPLICATION NATE: 12.48PH1.1991
## PRIOR APPLICATION NATE: 12.48PH1.1992
## PRIOR APPLICATION NATE: 13.48PH1.1992
## PRIOR APPLICATION NATE: 13.48PH1.1993
## PRIOR APPLICATION NATE: 13.49PH1.1993
## P
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RESULT 15
US-09-21-927-27
i Sequence 27, Application US/09911927
i GENERAL INFORMATION: ESERIAL FUNDAL GENES AND THEIR USE
i TITLE OF INVENTION: ESSENITAL FUNDAL GENES AND THEIR USE
i TITLE OF INVENTION NUMBER: US/09/911,927
CURRENT APPLICATION NUMBER: US/09/911,927
CURRENT FILING DATE: 1997-11-07
i PRIOR FILING DATE: 1997-11-07
i NUMBER OF SEQ ID NOS: 35
i SOFTWARE: FastSEQ for Windows Version 3.0
i SEQ ID NO 27
LENGTH: 62
i FATURE:
i OTHER INFORMATION: primer for PCR
is OTHER INFORMATION: primer for PCR
is OTHER INFORMATION: primer for PCR
US-09-911-927-27

QUELY MACCH SIMIlarity 38.5%; Pred: NO. 1.90+03;
Best Local Similarity 38.5%; Pred: NO. 1.90+03;
MATCHOS 20; CONSERVATIVE 11; Mismatches 21; Indels 0; Gaps 0;
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Search completed: October 16, 2006, 14:34:12 Job time : 111 sec8

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US-10-310-914A-16611/c
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-16611
                                       117.8
117.8
117.8
117.8
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1: FBMC Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /BMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /FBMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: FBMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
5: /BMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
10: /FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
11: /FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /FBMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
13: /FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
14: /FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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15: /FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /FBMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4883, Ap Sequence 288, App Sequence 288, App Sequence 288, App Sequence 188, App Sequence 137, Ap Sequence 22, Appl Sequence 12, Appl Sequence 15, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Appl
Sequence 3, Appli
Sequence 3993, Ap
                                                                                          ; Search time 881 Seconds
(without alignments)
1101.842 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16611,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                1 ggagggggggggagagacga......ucucuccuuucgccaccucc
           GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-849-928-4883
US-09-849-928-88
US-10-066-960-288
US-10-409-627-288
US-10-409-527-288
US-10-498-530-288
US-10-488-530-6
US-10-983-965-1187
6 US-11-106-909-22
6 US-11-228-636-23
1 US-10-918-636-31
US-10-918-740-15
US-09-918-740-15
US-10-835-516-15
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US-10-853-774-3
                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                 nucleic search, using sw model
                                                                                             October 16, 2006, 14:32:38
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Match Length DB
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Maximum DB seq length: 100
                                                                                                                                                 Title:
Perfect score:
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Sequence 16611, Application US/10310914A
Publication No. US20060003322A1
Publication No. US2006000332A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Laigudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
                                                                                 Sequence 27, Appl Sequence 27, Appl Sequence 1520, Appl Sequence 1520, Appl Sequence 10452, A Sequence 931, Appl Sequence 931, Appl Sequence 214, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 36, Appl Sequence 976170, Sequence 976170,
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Sequence 8102, Ap
Sequence 29840, A
Sequence 10, Appl
Sequence 24937, A
Sequence 173876,
Sequence 47265, A
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                                                                               US-09-911-888-27

US-09-911-888-27

US-10-26-734-458-51

US-10-310-914A-15206

US-11-175-859-73819

US-09-908-975-10452

US-09-908-975-931

US-09-908-975-931

US-10-286-734-314

US-10-286-734-314

US-10-286-734-314

US-10-286-734-314

US-10-286-734-314

US-10-286-734-314

US-10-286-734-288

US-10-286-734-288

US-10-286-734-288

US-10-91-55-55

US-10-91-55-56

US-10-91-56-56

US-11-686-58-363

US-10-964-549-363

US-10-964-549-363

US-11-036-317-976370

US-11-036-317-976370
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US-11-175-859-29840
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; Sequence 4883, Application US/09294093B

; Parcent No. US20010051335A1

; GRERAL INFORMATION:

; APPLICANT: Lalgudi, Raghunath, V.
    Query Match
Best Local Similarity 80.0
Matches 28; Conservative
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79 C 79
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                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 GGGGAGAGAGGGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCCUU 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGNGAGTCCGCTGGNAGTTNCCCATGAANNCTATNTNGANCTCGCTCGACCTCGCCGA 14
                                                                                                                                                                                                                                                                        , NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700355274H1
; NAME/KEY: unsure
; LOCATION: 32, 35, 37, 42-43, 52, 57, 69, 79, 81
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-4883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TOTLE OF SEQUENCES: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
COMPUTER: IBM pc compatible
SOFFRARING SYSTEM: MS-DOS
SOFFRARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 29.1%; Score 23; DB 3; I Best Local Similarity 43.7%; Pred. No. 2.2e+02; Matches 31; Conservative 7; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/849,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-May-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/42,793
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
FILING DATE: 07-JUNE-1995
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE: PERL Program
SEQ ID NO 4883
LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-849-928-288/c
; Sequence 288, Application US/09849928
; Publication No. US20030059769A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (303) 793-3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 UCGCCACCUCC 79
                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
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LENGTH: 97 base pairs
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US-10-705-300-288/c
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                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                           셤
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                                                                                                                                                                                                                                                                                                                                                                                                90 GTGAGCCTCCTGTCGAATCTTACTACTTCTGCTTTGTGTTTTGTTTCCTTGCGTGCCCCTT 31
                                                                                                                                                                                                                                                                                   Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 288, Application US/10409627
Publication No. US20040043923A1
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TO LECTINS
NUMBER OF SEQUENCES: 390
                                                                                                                                                                                                                                                                                                                            26; Indels
                                                                                                                                                  OTHER INFORMATION: All C's are 2'-NH2 cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB COMPUTER: IBM pc compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.0
                                                                                                                                                                                             OTHER INFORMATION: All U's are 2'-NH2 uracil
SEQUENCE DESCRIPTION: SEQ ID NO: 288:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 B. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
                                                                                                                                                                                                                                                                                 24.6%; Score 19.4; DB 6; 31.1%; Pred. No. 5.1e+03; iive 16; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/952,793
FILING DATE: 20-NOVEMBER-1997
APPLICATION NUMBER: PCT/US6/09455
FILING DATE: 05-JUNE-1995
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/477,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/409,627
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-JUNE-1995
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INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
                      LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
SEQUENCE CHARACTERISTICS
LENGTH: 97 base pai
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-10-409-627-288/c
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                                                                                                                                                                         FEATURE:
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                                                                                                                                FEATURE
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19 GAGGGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCCUUUCGCCACCUC 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.6%; Score 19.4; DB 8; Length 97; Best Local Similarity 31.1%; Pred. No. 5.1e+03; Matches 19; Conservative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 288, Application US/10705300
Publication No. US20040072234A1
GENERAL INPORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TO LECTINS
                                                                                                                                                                                      OTHER INFORMATION: All C's are 2'-NH2 cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
                                                                                                                                                                                                                                   OTHER INFORMATION: All U's are 2'-NH2 uracil SEQUENCE DESCRIPTION: SEQ ID NO: 288: US-10-409-627-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 B. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM DE COMPATIBLE
COMPUTER: IBM DE COMPATIBLE
COPERATING SYSTEM: MS-DOS
SOFTWARE: WORDER: G.O.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/705,300
FILING DATE: 10-Nov-2003
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/952,793
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: OF-JUBE-1995
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
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REFERENCE/DOCKET NUMBER: NEX40C/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Barry J. Swanson
LENGTH: 97 base pairs
                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 288
                                                                                           TOPOLOGY: linear
                                                                                                                     MOLECULE TYPE: RNA
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4 GGGCGGGGGGAGCGAGCGGCCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUU 62
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APPLICANT: STHARBE, MICHAEL
APPLICANT: SIDDIQUI-JAIN, Adam
APPLICANT: SIDDIQUI-JAIN, Adam
APPLICANT: MORAN, TETENCE
TITLE OF INVENTION: SUBSTITUTED QUINOBENZOXAZINE ANALOGS AND
TITLE OF INVENTION: METHODS OF USING THEREOF
FILE REFERENCE: 532232001121
CURRENT APPLICATION NUMBER: US 10/903,975
PRIOR FILING DATE: 2004-01-15
PRIOR APPLICATION NUMBER: US 10/903,975
PRIOR PLILING DATE: 2004-04-07
PRIOR PLILING DATE: 2004-04-07
PRIOR FILING DATE: 2004-07-07
PRIOR FILING DATE: 2003-04-15
PRIOR FILING DATE: 2003-04-15
PRIOR FILING DATE: 2003-04-15
PRIOR FILING DATE: 2003-04-15
PRIOR FILING DATE: 2003-11-12
PRIOR FILING DATE: 2003-11-12
PRIOR FILING DATE: 2003-11-12
PRIOR FILING DATE: 2003-11-12
PRIOR FILING DATE: 2003-11-23
NUMBER OF SEQ IO NUMBER: US 60/532,727
PRIOR FILING DATE: 2003-11-23
NUMBER OF SEQ IO NOS: 22
TENNAME: FASTESQ FOR WINGOWS VEFSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 24.1%; Score 19; DB 16; Length 86 I Similarity 42.4%; Pred. No. 7.1e+03; 25; Conservative 9; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 CCCCUDAAUGUACUUCGGCUCGUAUUGUCUCUCCUUUC 70
                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: Clone ID: 23-LIB2809-008-Q1-E1-F3
US-09-983-965-1387
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.3%; Score 19.2; DB 3; Best Local Similarity 37.5%; Pred. No. 5.9e+03; Matches 15; Conservative 12; Mismatches 13;
     MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITIFIED REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965;
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1996-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/11106909
Publication No. US20060029950A1
GENERAL INFORMATION:
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; Publication No. US20060074089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jeffrey P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WHITTEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-11-228-636-22
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                                                                                                                                                                                                                                                                   LENGTH: 87
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Patent No. US20020137160A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byat.v. John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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; Sequence 6, Application US.0040018530A1
; GENERAL INFORMATION:
    APPLICANT: Bowser, Michael T
    APPLICANT: Bowser, Michael T
    APPLICANT: Mendonas, Shaun D
    TILE OF INVENTION: IN VITRO EVOLUTION OF FUNCTIONAL RNA AND DNA USING
    TILE OF INVENTION: LEECTROPHORETIC SELECTION
    TILE OF INVENTION: ELECTROPHORETIC SELECTION
    TILE OF INVENTION: ELECTROPHORETIC SELECTION
    TILE OF INVENTION: LO 01870101
    CURRENT APPLICATION NUMBER: 06/344,709
    PRIOR FILING DATE: 2003-05-29
    PRIOR PELICATION NUMBER: 60/470,750
    PRIOR APPLICATION NUMBER: 60/470,750
    PRIOR FILING DATE: 2003-05-15
    NUMBER OF SEQ ID NOS: 127
    SOFTWARE: Patentin version 3.2
    SEQ ID NO 6
    LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                           19 GAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCCUUUCGCCACCUC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 GCGGGGGAGAGACGAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUC 65
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                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                         Query Match 24.6%; Score 19.4; DB 8; Length 97; Best Local Similarity 31.1%; Pred. No. 5.1e+03; Matches 19; Conservative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 24.3%; Score 19.2; DB 8; Length 80; Best Local Similarity 35.9%; Pred. No. 5.9e+03; Matches 23; Conservative 13; Mismatches 28; Indels
                                                                                                                                    All C's are 2'-NH2 cytosine
                                                                                                                                               OTHER INFORMATION: All U's are 2'-NH2 uracil SEQUENCE DESCRIPTION: SEQ ID NO: 288:
     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                    OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: aptamer US-10-448-250-6
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US-09-983-965-1387
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                                                                                                            FEATURE
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US-10-448-250-6
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Sequence 15, Application US/09918740
Publication No. US20030033626A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hahn, Frederick
APPLICANT: Kuchnle, Adelheid
TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways to TITLE OF INVENTION: create novel traits in transgenic organisms
FILE REFERENCE: KAS-103XC1
CURRENT APPLICATION NUMBER: US/09/918,740
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            Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT AFFE: DESCRICE
COMPUTER: IBM Compatible
COERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,123
FILING DATE: 04-Apr-2003
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/367,791A
FILING DATE: 12-No: US/20/367,791A
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: MT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
FILING DATE: 27-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 CCUUAAUUGUACUUCGGCUCGUAUUGUCUCCUUUC 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 23.8%; Score 18.8; DB 7; Local Similarity 44.7%; Pred. No. 7.6e+03; nes 17; Conservative 9; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: DNA SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-10-407-123-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/221,703
PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
GENERAL INFORMATION:
APPLICANT: Himmelspach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-918-740-15/C
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FAPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 37212
LENGTH: 24
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42.4%; Pred. No. 7.1e+03;
tive 9; Mismatches 25; Indels
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0; Mismatches
                                                                                                                                                                                                     TITLE OF INVENTION: QUINOLONE ANALOGS
FILE REFERENCE: 532232001820
CURRENT APPLICATION NUMBER: US/11/228,636
CURRENT FILING DATE: 2005-09-16
PRIOR APPLICATION NUMBER: US 60/611,030
PRIOR PILING DATE: 2005-06-09
PRIOR PILING DATE: 2004-09-17
PRIOR FILING DATE: 2004-10-17
PRIOR FILING DATE: 2004-10-27
PRIOR PILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 60/688,986
PRIOR PILING DATE: 2005-06-09
PRIOR PILING DATE: 2005-06-09
PRIOR PILING DATE: 2005-06-09
PRIOR PILING DATE: 2005-06-09
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SOFTWARE: FastSEQ for Windows Version 4.0
                   WHITTEN, Jeffrey P.
PIERRE, Fabrice
REGAN, Collin
SCHWAEBE, Michael
YIANNIKOUROS, George Petros
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                                                                                                                                       JUNG, Michael
NAGASAWA, Johnny Y.
CHUA, Peter
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Best Local Similarity 42.44
Them 25; Conservative
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Best Local Similarity 90.9
Matches 20, Conservative
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LENGTH: 86
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| Bublication No. US20050241017A1
| GENERAL INFORMATION:
| APPLICANT: Hahn, Frederick
| APPLICANT: Hahn, Frederick
| TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways to TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways to TITLE OF INVENTION: CREATE novel traits in transgenic organisms
| TITLE OF INVENTION: CREATE novel traits in transgenic organisms
| TITLE OF INVENTION: CREATE novel traits in transgenic organisms
| TITLE OF INVENTION: UNMBER: US/11/053,541
| CURRENT FILING DATE: 2005-02-08
| PRIOR FILING DATE: 2001-07-31
| PRIOR FILING DATE: 2001-07-31
| PRIOR FILING DATE: 2000-07-31
| PRIOR FILING DATE: 2000-07-31
| MUBBER OF SEQ ID NOS: 76
| SOFTWARE: Patentin Version 3.0
| SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    volutional control of Application US/10835516

publication No. US20040194162A1

is Geguence 15, Application US/10835516

publication No. US20040194162A1

is GENERAL INFORMATION:

APPLICANT: Hahn, Frederick

APPLICANT: Kuchnle, Adelheid

TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways tritle OF INVENTION: create novel traits in transgenic organisms

TITLE OF INVENTION: Create novel traits in transgenic organisms

TITLE OF INVENTION: QUARER: 2004-04-28

CURRENT APPLICATION NUMBER: US/10/835,516

PRIOR PRILING DATE: 2001-07-31

PRIOR FILING DATE: 2000-07-31

PRIOR FILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 76

SOFTWARE: PatentIn version 3.0

SEQ ID NO 15

LENTH: 72

LENTH: 72
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US-09-918-740-15
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                                                                                                                                                                                                                                                                      Length 72;
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NUMBER OF SEQ ID NOS: 76
SOFWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 72
                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Matches 13; Conservative
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Matches 13; Conservative
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US-11-053-541-15/c
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US-10-835-516-15/c
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Published Applications NA New:*

| EMC Celerra SIDS3/ptodata/2/pubpna/USO9 NEW PUB.seq:*
| FMC Celerra SIDS3/ptodata/2/pubpna/USO6 NEW PUB.seq:*
| FMC Celerra SIDS3/ptodata/2/pubpna/USO7 NEW PUB.seq:*
| FMC Celerra SIDS3/ptodata/2/pubpna/USO8 NEW PUB.seq:*
| FMC Celerra SIDS3/ptodata/2/pubpna/PCT NEW PUB.seq:*
| FMC Celerra SIDS3/ptodata/2/pubpna/PCT NEW PUB.seq:*
| FMC Celerra SIDS3/ptodata/2/pubpna/USI NEW PUB.seq:*
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9715, Ap
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648, App
25, Appl
9, Appli
618728,
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403, App
10, Appl
216548,
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5, Appli
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(without alignments)
1061.937 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-348-413-425880
US-11-348-413-425881
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                                                                                                                                                                                                                                                       2395520 segs, 934235491 residues
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Maximum Match 100%
Listing first 45 summaries
                                                        nucleic search, using sw model
                                                                                      October 16, 2006, 14:34:29
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Maximum DB seq length: 100
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Match
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Perfect score:
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                                                          nucleic
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16.2 16.2 16.2 16.2 16.2 16.2 16.2 16.2	15.08	RESULT 1 US-11-217-529-173876 Sequence 173876, App Publication No. US20 GENERAL INFORMATION: APPLICANT: SUNTORY APPLICANT: NAKAO, APPLICANT: KODAWA, APPLICANT: KODAWA, APPLICANT: KODAWA, APPLICANT: KODAWA, APPLICANT: ASHIKAR TITLE OF INVENTION: FILE REFERENCE: S-7 CURRENT APPLICATION CURRENT APPLICATION CURRENT APPLICATION CURRENT APPLICATION SPRIOR APPLICATION FILE REFERENCE: S-7 FILE ON 173876 LENGTH: 99 LENGTH: 90 LENGTH: 9	-529- atch cal S 139
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Sequence 1090, Application US/11143642
Publication No. US20060099610A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD AND KIT FOR DETECTING A RISK OF ACUTE MYOCARDIAL INFARCTION
FILE REFERENCE: 0933-0245FUS1
CURRENT APPLICATION NUMBER: US/11/143,642
CURRENT FILING DATE: 2005-06-03
NUMBER OF SEQ ID NOS: 2039
SOFTWARE: Patentin version 3.3

RESULT 2 US-11-143-642-1090

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US-10-526-765-9/c
; Sequence 9, Application US/10526765
; Publication No. US20060121049A1
; GENERAL INFORMATION:
                                              ch 23.0%;
.1 Similarity 48.4%;
15, Conservative 6
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Best Local Similarity 35.6
Matches 16; Conservative
                                                 Query Match
Best Local Similarity
Matches 15; Conserv
US-10-554-759-648
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; Sequence 648, Application US/10554759
; Sequence 648, Application US/10554759
; Publication No. US200601778251
; Publication No. US200601778251
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: Cells
; TITLE OF INVENTION: Cells
; FITLE OF INVENTION NUMBER: 60/466,801
; CURRENT APPLICATION NUMBER: 60/466,801
; PRIOR APPLICATION NUMBER: 60/466,801
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FREESEQ FOR Windows Version 4.0
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Fublication No. US20060115806A1

Fublication Not Inversity of Georgia Research Foundation

FILE OF INVENTION: Global Analysis of Transposable Elements

FILE OF INVENTION: as Molecular Markers of Cancer

FILE REFERENCE: 21099,0075P1

CURRENT APPLICATION NUMBER: US/10/554,711

CURRENT APPLICATION NUMBER: US/10/456,798

FRIOR PILING DATE: 2003-04-29

FRIOR PILING DATE: 2003-04-29

NUMBER OF SEQ ID NOS: 778

SEQ ID NO 648

LENGTH: 50
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                                                                                                                                                Query Match 23.3%; Score 18.4; DB 8; Length 51; Best Local Similarity 41.3%; Pred. No. 2e+03; Matches 19; Conservative 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: Description of Artificial Sequence:/note; OTHER INFORMATION: Synthetic Construct
US-10-554-711-648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 50;
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Pred. No. 2.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 TTGGGACTCGGACTGCTCTTGCTCTC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.0%;
Best Local Similarity 48.4%;
Matches 15; Conservative
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                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-11-143-642-1090
                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-10-554-711-648
SEQ ID NO 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 648
LENGTH: 50
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TITLE OF INVENTION: CHIMERIC RECOMBINANT PROTEIN AND IN VITRO DIAGNOSIS
FILE REPERRENCE: 122802
CURRENT APPLICATION NUMBER: US/10/526,765
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: PCT/FR03/02712
PRIOR APPLICATION NUMBER: PC1/FR03/02712
PRIOR APPLICATION NUMBER: P02/11485
PRIOR PILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.3
SEQ ID NO 9
LENGTH: 90
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                     RESULT 5

US-11-357-615-25

Sequence 25, Application US/11357615

Publication No. US20060188972A1

GENERAL INFORMATION:

APPLICANT: WOLFFE, Alan P.

APPLICANT: COLLINGWOOD, Trevor

TITLE OF INVENTION: TARGETED MODIFICATION OF CHROMATIN STRUCTURE

FILE REFERENCE: 8325-0014 / S14-US1

CURRENT APPLICATION NUMBER: US/09/844,508

PRIOR FILING DATE: 2006-02-16

PRIOR APPLICATION NUMBER: US/09/844,508

PRIOR APPLICATION NUMBER: 00/200,590

PRIOR APPLICATION NUMBER: 60/200,590

PRIOR FILING DATE: 2000-04-28

INWHERE OF SEQ ID NOS: 49

SEQ ID NO 25

ILENGTH: 77
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     Length 50;
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                                                            Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: encoding DGGGS linker, 3' to 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TGTAGTTTTGGGTGGTCTTGTTCTTTCTGCCGCCACC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 uguacuuceeecuceuauugucuccuccuuuceccace 76
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Score 18.2; DB 6;
Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.5%; Score 17.8; DB 7;
37.8%; Pred. No. 3.8e+03;
trive 11; Mismatches 12;
                                                                                                                                               12 TIGGGACTCGACTGGCTCTCCTTGCTCCTC 42
                                                                                                               45 UNCEGECUCEUAUUGUCUCCUUUCGCCAC 75
                                                         8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human immunodeficiency virus type US-10-526-765-9
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                                                                                                                                                                                                                                                       Gaps
                                                         FEATURE:
; OTHER INFORMATION: Reverse primer sequence used to amplify XptB1 US-11-375-551-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JUSTICAL STATEMENT OF THE PROPERTY OF THE PROP
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Publication No. US20060183106A1
GENERAL INFORMATION:
APPLICANT: SIDDIQUI-JAIN, Adam
TITLE OF INVENTION: QUADRUPLEX-TARGETED ANTIVIRAL MOLECULES
FILE REPERENCE: 332222000900
CURRENT APPLICATION NUMBER: US/10/531,545
                                                                                                                                                                                 Query Match
21.8%; Score 17.2; DB 9; Length 66;
Best Local Similarity 36.8%; Pred. No. 6e+03;
Matches 14; Conservative 11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 76;
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                                                                                                                                                                                                                                                                                                                                                     24 GCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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Best Local Similarity 51.4%; Pred. No. 6.3e+03;
Matches 18; Conservative 4; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
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NAME/KEY: misc feature
LOCATION: 7, 11, 18, 30, 31, 46, 47, 61,
COTHER INFORMATION: n = A,T,C or G
US-11-374-388-403
TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-374-388-403
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                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mounte, william M
APPLICANT: Mounte, william M
APPLICANT: Mounte, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (Am 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2005-10-05
PRIOR PILING DATE: 2005-10-05
PRIOR PILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 618728
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APPLICANT: Schafer, Barry
APPLICANT: Guo, Lining
TITLE OF INVENTION Xenorhabdus TC Proteins and Genes for Pest Control
FILE REFERENCE: DAS-105X
CURRENT APPLICATION NUMBER: US/11/375,551
CURRENT APPLICATION NUMBER: US/10/753,901
PRIOR APPLICATION NUMBER: US 60/441,717
PRIOR APPLICATION NUMBER: US 60/441,717
PRIOR PILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.3
SEQ ID NO 85
LENGTH: 66
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| NAME/KEY: misc_feature
| LOCATION: (1)..(25)
| OTHER INFORMATION: SEQ ID NO: 370; WANOIUJA4-5_at; Start 75; Stop 99;
| OTHER INFORMATION: 011101100000000
| US-11-348-413-618728
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                            3; Indels
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21.8%; Score 17.2; DB 9;
Best Local Similarity 40.9%; Pred. No. 4.5e+03;
Matches 9; Conservative 10; Mismatches 3;
                                                                                                                                                                                                                                       Sequence 618728, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
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APPLICANT: Mitchell, Jon
APPLICANT: Larrinua, Ignacio
APPLICANT: Apel-Birkhold, Patricia
APPLICANT: Schafer, Barry
APPLICANT: Schafer, Barry
APPLICANT: Young, Scott
APPLICANT: Guo, Lining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 GCUCGUAUUGUCUCCUCCUUUCG 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: probe
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                                                                                                                                                                             RESULT 7
US-11-348-413-618728/c
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GAPLICANT: Cohen, Joniel
APPLICANT: Cohen, Joniel
APPLICANT: Cohen, Joniel
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high
TITLE OF INVENTION: Biallelic markers for use in constructing a high
TITLE OF INVENTION: Gensiev...
FILE REFERENCE: GENSET. 0206-03-08
CURRENT FILING DATE: 2003-03-08
PRIOR FILING DATE: 2003-03-03
PRIOR PLILING DATE: 1999-10-20
PRIOR PLILING DATE: 1999-10-20
PRIOR PLILING DATE: 1999-10-20
PRIOR PLILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1998-04-21
PRIOR FILING DATE: 1998-04-21
PRIOR FILING DATE: 1998-04-21
PRIOR FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 3264
LENGTH: 47
TAPPLED
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Pred. No. 6.4e+03;
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21.5%; Score 17; DB 8; Length 93;
Best Local Similarity 31.7%; Pred. No. 7.9e+03;
Matches 13; Conservative 13; Mismatches 15; Indels
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Publication No. US20060112449A1

GENERAL INFORMATION

APPLICANT: Van der Linden, C.G.

APPLICANT: Alwee, Sharifah S.R.S.

APPLICANT: Choo, Cheah S.

TITLE OF INVENTION: NOVEL B-type gene from oil palm

FILE REFERENCE: SHOEL2. 002AUS

CURRENT FILING DATE: 2005-09-30

PRIOR FILING DATE: 2004-09-30

PRIOR FILING DATE: 2004-09-30

NUMBER: OF SEQ ID NOS: 26

SEQ ID NO S.

LENGTH: 93

LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele

... LOCATION: 24

... COCATION: 24

... CTHER INFORMATION: 99-2832-152 : polymorphic base C or US-11-370-584-3264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTGCCCCTTCTATCTCTCTGGTGTCTTTCTCTC 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.5%;
  Publication No. US20060177863A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Elaeis guineensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo Sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-243-296A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mounts, william M
APPLICANT: Mounts, william M
APPLICANT: Mounts, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031866-084400 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR PILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
PRIOR FILING DATE: 2004-10-05
PRIOR PILING DATE: 2004-10-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 GGAGGGTGGGGAGGGTGGGAAGGTTAGCGACACGCAATTGCTATAGTGAGTCGTATTAG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGAGGGCGCGCGGAGAGACGACCGCCUCUGCCCCUUAAUUGUACUUCGGGCUCGUAUUGU 60
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21.8%; Score 17.2; DB 6; Length 99;
Best Local Similarity 40.3%; Pred. No. 6.8e+03;
Matches 25; Conservative 9; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.5%; Score 17; DB 9; Length 25; 36.0%; Pred. No. 5.3e+03; tive 11; Mismatches 5; Indels
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: PCT/US03/33366
PRIOR FILING DATE: 2003-10-20
PRIOR PRIOR APPLICATION NUMBER: US 60/419,456
PRIOR FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-348-413-216548/c
; Sequence 216548, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 UAAUUGUACUUCGGGCUCGUAUUGU 60
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US-11-370-584-3264/c
; Sequence 3264, Application US/11370584
                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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Best Local Similarity 36.0%;
Section 9; Conservative
                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Primer US-10-531-545-10
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OTHER INFORMATION: probe
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APPLICANT: Murphy, Bilan M
APPLICANT: Murphy, Bilan M
APPLICANT: Murphy, Bilan
APPLICANT: Murphy, Bilan
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: US/11/348,413
FRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR APPLICATION NUMBER: US 60/615,573
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 216546
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APPLICANT: Wounts, William M
APPLICANT: Wounts, William M
APPLICANT: Wounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 03406-084100 (Am 10.1724)
CURRENT PELING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR PELING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
NUMBER: OF SEQ ID NOS: 1276209
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; NAME/KEY: misc feature
; LOCATION: (1)...[425]
; OTHER INFORMATION: SEQ ID NO: 6358; WANOIUKNQ; Start 1513; Stop 1537;
; OTHER INFORMATION: 000000011100000
US-11-348-413-216546
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... OTHER INFORMATION: SEQ ID NO: 6358; WANDIUKNO; Start 1514; Stop 1538;
... OTHER INFORMATION: 000000011100000
US-11-348-413-216547
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21.0%; Score 16.6; DB 9; Length 25;
Best Local Similarity 39.1%; Pred. No. 7.5e+03;
Matches 9; Conservative 10; Mismatches 4; Indels
Sequence 216546, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
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Publication No. US20060160121A1
GENERAL INFORMATION:
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OTHER INFORMATION: probe
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LOCATION: (1)..(25)
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LENGTH: 25
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   Length 25;
                                        4; Indels
Query Match
21.0%; Score 16.6; DB 9;
Best Local Similarity 39.1%; Pred. No. 7.5e+03;
Matches 9; Conservative 10; Mismatches 4;
                                                                          38 AUUGUACUUCGGCUCGUAUUGU 60
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24 ATTGTAATTCTGGATGGTATTGT 2
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Search completed: October 16, 2006, 14:51:29 Job time : 140 secs

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Add985989 S.tuberos Adi94592 Murine IF Aex56946 HIV-1 pro Aef05103 Human Mu/ Adc05103 Human Na/ Adc05109 Human Na/ Adc05108 Human Na/ Adc05108 Human Na/ Adc05107 Human all Aec26021 Human all Aec26021 Human all Aec26021 Human all Ac27983 VIC/ET-1/ Ada09553 Murine ET Ada09553 Murine ET Ada05597 Human all Ac416088 Human mic Ac416088 Human all Ac416088 Human adi Adc01938 Human adi

Scoring table:

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Minimum Maximum

Database

Title: Perfect score:

Sequence:

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The present invention relates to a method for diagnosing disease or predisposition to a disease, associated with a disease causing mutations in a retinitis pigmentosa GTPase regulator (RPGR) gene involves genotyping a RPGR gene, and determining whether the genotype comprises a disease causing mutations, where the risk genotype is present within open
                                                                                                                                                                                                                                                                                                                                                                  Human; mutation; retinitis pigmentosa GTPase regulator; RPGR; genotyping; open reading frame; ORF; X-linked retinitis pigmentosa; XLRP; gene therapy; screening; forensic analysis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing disease or predisposition to disease, associated with disease causing mutations in retinitis pigmentosa GTPase regulator gene by genotyping ORF15 of the gene, and determining presence of mutations.
                                                                                                                                                                                                                                                                                                                                                    Imperfect direct repeat #1 of human RPGR exon ORF15 repetitive sequence.
                                                                                                                                                                                                                                                       ALIGNMENTS
         ADI94592
AAX56946
AEF13105
ADC05103
ADC05104
ADC05108
ADC05108
ADC05108
ADC05108
AAA038850
AAA038850
AAA038850
AAA038850
AAA03850
AAA038727
AAX04071
AAA488099
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AAC070938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-2001; 2001WO-GB001622
                 (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                 AAD21686 standard; DNA; 24
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WO200177380-A2
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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13.8
13.8
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AAD21686/c
Aee94315 3' primer
Adi94591 Murine IF
Adi94590 Murine IF
Adi94590 Murine IF
Adi94580 Murine IF
Aav91451 Human C-r
Aaf01081 Hammerhea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aaq44801 Purine-ri
Aaq44806 Oligonucl
Aat99274 Human PUR
Aav31726 Nucleotid
Aax41731 Nucleotid
Aax4070 Oligonucl
Aax64070 Oligonucl
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- 2006 Biocceleration Ltd
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Maximum Match 100%
Listing first 45 summaries
                                         - nucleic search, using sw model
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AAQ4801
AAQ44801
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                                                                                                                                                                                         seq length: 0
seq length: 30
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Match
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Adx99968 PCR prime Aaq65826 Type II p Adi94593 Murine IF

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Score 15.6; DB 2; Pred. No. 4.5e+03; 7; Mismatches 4;

65.0%;

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Query Match Best Local Similarity Matches 11; Conserv

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23 TTTTCTCCCTCCACCACCTC 2

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AAQ44806 standard; DNA; 24

RESULT 3 AAQ44806

24;

Oligonucleotide MR0700 used in characterising c-myc PUR element.

(first entry)

(revised)

25-MAR-2003 28-SEP-1994

AAQ44806;

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reading frame (ORF)15 of the RPGR gene. The method is useful for detecting a certain disease state e.g., X-linked retinitis pigmentosa (XLRP). The kit is useful for detecting and measuring disease causing mutations in biological fluids and tissues and for localising mutation in tissues. The mutant RPGR gene is useful in gene therapy techniques and tosues. The mutant RPGR gene is useful in gene therapy techniques and and/or the biological activity of mutant RPGR. They are preferably useful for identifying agonists and antagonists of RPGR. The mutant RPGR gene is also useful in identification of potential pharmaceutical targets in high throughput screening assays and forensic analysis. The present sequence is the imperfect direct repeat of human RPGR exon ORFIS repetitive DNA
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single-strand binding protein; PUR protein; cellular oncogene; eukaryotic origin of replication; gene amplification; cancer cell; retinoblastoma protein; helix-destabilising protein; inhibitor; hyperproliferation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning and expression of PUR protein, involved in regulation of replication - also oligo:nucleotide(s) and antibodies for use in treatment of proliferative diseases, e.g. cancer.
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                                                                                                                                                                                                                    Match 65.8%; Score 15.8; DB 4; Length 24; Local Similarity 52.6%; Pred. No. 3.7e+03; les 10; Conservative 7; Mismatches 2; Indels
                                                                                                                                                                                          Sequence 24 BP; 10 A; 0 C; 14 G; 0 T; 0 U; 0 Other;
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19 TCTCTCCTTTCCCCTCCTC
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purine-rich PUR element.
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28-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                  Cloning and expression of PUR protein, involved in regulation of DNA replication - also oligo:nucleotide(s) and antibodies for use in the treatment of proliferative diseases, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                           Single-strand binding protein; PUR protein; cellular oncogene; eukaryotic origin of replication; gene amplification; cancer cell; retinoblastoma protein; helix-destabilising protein; inhibitor; hyperproliferation; c-myc; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.0%; Score 15.6; DB 2; Length 24; 50.0%; Pred. No. 4.5e+03; ive 7; Mismatches 4; Indels
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Best Local Similarity
Matches 11, Conserv
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PUR elements are purine-rich 24 nucleotide DNA sequences which occur at everaryotic origins of replication and 5' flanking regions of some cellular oncogenes. The PUR procesin (ARR50310) was originally identified as a 27kD HeLa cell nuclear factor that bound in a sequence-specific manner to a major site of DNA bending located 1.6kb upstream of the transcription start site of the human c-myc gene; the site recognised by PUR protein had the sequence AAQ44801. (Updated on 25-MAR-2003 to correct

Claim 6; Page 65; 97pp; English

Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;

Gaps

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This is the nucleotide sequence of the PUR element used in the method of the invention, involving the use of the PUR protein and its fragments, which inhibit PUR protein binding to PUR element or other proteins. Inhibitors of PUR activity may be useful for treating viral infections and hyperproliferative diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the nucleotide sequence of an oligonucleotide used in the method of the invention, involving the use of the PUR protein and its fragments, which inhibit PUR protein binding to PUR element or other proteins inhibitors of PUR activity may be useful for treating viral infections
                                                                                    PUR protein and its fragments - that inhibit PUR protein binding to PUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein and its fragments - that inhibit PUR protein binding to PUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUR-alpha gene; inhibition; viral infection; cancer; PUR element; hyperproliferative disease; ss.
                                                                                                                                                                                                                                                                        Query Match 65.0%; Score 15.6; DB 2; Length 24; Best Local Similarity 50.0%; Pred. No. 4.5e+03; Matches 11; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.6; DB 2; Length 24; Pred. No. 4.5e+03;
                                                                                                                                                                                                                                               Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of the oligonucleotide MR0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and hyperproliferative diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6.1.1; Col 27; 63pp; English
(MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                   3 UNGUCUCUCCUTUCGCCACCUC 24
                                                                                                                              Disclosure, Col 12, 63pp, English.
                                                                                                                                                                                                                                                                                                                                                  23 TTTCTCTCCCTCCACCACCTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00470911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-00938189.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV31731 standard; DNA; 24
                            Johnson EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              element or other proteins.
                                                                                                    element or other proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson
                                                       WPI; 1998-321632/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-321632/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bergemann AD,
                            Bergemann AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5756684-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV31731;
                                                                                                                                                                                                                                                                                                                                                                                                                       AAV3173
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
 8X1X8X11X8X00000X8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                              Assays for PUR protein ligands or modulators - using immobilised PUR protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                  The probes AAT99270-T99277 were used to screen for positive clones containing a 467 bp Sau3AI fragment of the human c-myc upstream region cloned into pUC19. Isolated sequences were then used as probes to screen an expression library for sequences encoding the PUR protein. The PUR sequence can be used to identify chemical or biological compounds that bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may be used to treat hyperproliferative diseases such as cancer
                                        PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss; cancer; probe; hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
hyperproliferative disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 65.0%; Score 15.6; DB 2; Length 24; Best Local Similarity 50.0%; Pred. No. 4.5e+03; Matches 11; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of the PUR element.
                                                                                                                                                                                                                                                                          (MOUN ) MOUNT SINAI SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TITICICICCICCACCACCTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 unguencuccunucgecaecuc 24
               Human PUR-alpha gene probe MR0700
                                                                                                                                                                                                                                                                                                                                                                                                         Example, Col 26, 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                              93US-00014943.
95US-00470911.
                                                                                                                                                                                     95US-00486421
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                                                                                                                                                                                                                  92US-00938189
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                                                                                                                                                                                                                                                                                                      Bergemann AD, Johnson EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV31726 standard; DNA;
                                                                                                                                                                                                                                                                                                                                   WPI; 1997-488859/45.
                                                                                                 Homo sapiens
                                                                                                                                                                                     07-JUN-1995;
                                                                                                                                                                                                                  28-AUG-1992;
                                                                                                                                                                                                                              02-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-1992;
02-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                            US5672479-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-1998
                                                                                                                                                         30-SEP-1997
                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV31726;
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Matches

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The present invention describes a monoclonal antibody that specifically binds to an epitope of the PUR protein. Antibodies that bind to the PUR protein and neutralise PUR activity may be used to treat hyperproliferative diseases such as cancer. PUR antibodies may be used diagnostically to detect aberrant expression of the PUR protein and/or mutations in the PUR apen. The present sequence represents an oligonucleotide used in the identification and characterisation of the PUR protein and its sequence element PUR repeat, in an example from the
Oligonucleotide MR0700 used in PUR identification/characterisation.
                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody specific for PUR protein - useful for treating
                                  PUR element; PUR-alpha; hyperproliferative disease; cancer; human; monoclonal antibody; identification; characterisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromatin; DNA hybridization; DNA amplification; DNA microarray; diagnosis; ss; primer; PCR; OLIG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels

    primer for PCR of DNase I treated OLIG2 chromatin.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 65.0%; Score 15.6; DB 2; Best Local Similarity 50.0%; Pred. No. 4.5e+03; Matches 11; Conservative 7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                 SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITICICCICCACCACCTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 unguencecommegeceaecue 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Col 27; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                            95US-00486809.
                                                                                                                                                                                                                                            92US-00938189
                                                                                                                                                                                                                                                             93US-00014943.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAY-2004; 2004US-0575478P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEE94315 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                   Johnson EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-152881/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2005118873-A2.
                                                                                                                                                                                                                                                                                                                                                   Bergemann AD,
                                                                                                                                                                                                                                                                                                                 TWUOM ( NUOM)
                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-FEB-2006
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                                                                                                                                                                                                            07-JUN-1995;
                                                                                                                                                                                                                                                                                06-JUN-1995;
                                                                                                                                                                                                                                                                  02-FEB-1993;
                                                                                                                                       US5869622-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-2005.
                                                                                                                                                                           09-FEB-1999
                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEE94315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a monoclonal antibody that specifically binds to an epicope of the PUR protein. Antibodies that bind to the PUR protein and neutralise PUR activity may be used to treat hyperproliferative diseases such as cancer. FUR antibodies may be used diagnostically to detect aberrant expression of the PUR protein and/or mutations in the PUR gene. The present sequence represents an oligonuclectide used in the identification and characterisation of the PUR protein and its sequence element PUR repeat, in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
     Gaps
                                                                                                                                                                                                                                                              Oligonucleotide MF0677 used in PUR identification/characterisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody specific for PUR protein - useful for treating
                                                                                                                                                                                                                                                                                                 PUR element, PUR-alpha, hyperproliferative disease, cancer; human, monoclonal antibody; identification; characterisation; ss.
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Pred. No. 4.5e+03;
7; Mismatches 4; Indels
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;
       4
     7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SINAI SCHOOL MEDICINE.
                                     3 UNGUCUCUCUTUCGCCACCUC 24
                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 UNGUCUCUCCUUUCGCCACCUC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITICICICCICCACCACCTC 2
                                                         rrrcrcrccrccaccaccrc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00486809
                                                                                                                                                           AAX04070 standard; DNA; 24
                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bergemann AD, Johnson EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0
Matches 11, Conservative
     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-152881/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ( MOUNT ) MOUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-1992;
02-FEB-1993;
06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-APR-1999
                                                                                                                                                                                                                              12-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                        US5869622-A
                                                                                                                                                                                                                                                                                                                                                                                                                                          09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                               AAX04070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX04075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer.
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RESULT 8
AAX04075
ID AAX0
XX
AC AAX0
XX
DT 12-A
XX

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Gaps

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Length 24;

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The new invention relates to detecting open circomatin in genomic DNA by determining the hybridization of acapture probe to a treated sample compilification products and the untreated sample amplification products and the untreated sample amplification products or Specifically, the method comprises preparing a chromatin sample with an open chromatin DNA cleaving agent or produce the chromatin sample with an open chromatin DNA cleaving agent to produce fragments; performing a first amplification reaction using the fragments as a substrate, to produce treated-sample amplification products; concerning a second amplification reaction using the fragments as a substrate, to produce treated-sample amplification products and the chromatin DNA cleaving agent, to produce untreated-sample amplification products and the chromatin DNA cleaving agent, to produce untreated-sample amplification products with a capture probe; and cerraming the hybridization of the capture probe; and determining the hybridization of the capture probe; and where reduced hybridization of the capture probe to the products amplification products with a capture probe; and where reduced hybridization of the capture probe to the capture probe; and where reduced hybridization of the capture probe to the intreated-sample amplification products as compared to the hybridization of the capture probe to the untreated-sample amplification products as compared to the hybridization of the capture probe to the untreated sample amplification of the capture probe to the untreated sample amplification products as compared to the hybridization of creatment in genomic DNA. The methods and chromatin state profiling array, for detecting the response of cells and patients to candidate corresponse to a useful for detecting open chromatin in genomic DNA. The methods and are useful for monitoring treatment and evaluating the response of cells and patients to capture profiling array or restablished therapeutic agents. The present sequence is a 3' reverse primer for one-said
                                                                                                                                                                                                                                                                                                                                               genomic DNA by
                                                                                                                                                                       Detecting open chromatin comprises determining hybridization of the capture probe to the treated- and untreated-sample amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.0%; Score 15.6; DB 15; Length 25; 40.9%; Pred. No. 4.5e+03;
                                                                                                                                                                                                                                                                                                                                               to detecting open chromatin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25 BP; 13 A; 0 C; 11 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
                                                                                                                                                                                                                                                                                      Example 1; Page 37; 43pp; English.
                                                                                                                                                                                                                                                                                                                                            The new invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 40.5.
Best Local 9; Conservative
                                                                                                              WPI; 2006-047578/05
(CEMI-) CEMINES INC
                                                        Neuman T;
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2 AUMGUCUCCUUUCGCCACCU 23 ઠે

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Gaps

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22 ATTCTCTCTTTTTCTCCTCT 1 셤

ADI94591 Standard; DNA; 21 (first entry) 04-NOV-2004 ADI94591; 

ВЪ.

Murine IFN-gamma associated probe SEQ ID 2144.

functional domain; nucleic acid cleavage assay; nuclease; polymerase;
detection; microorganism; RNA genome; hepatitis C;
human immunodeficiency virus; ss; probe.

Mus musculus.

29-NOV-2001.

WO200190337-A2

24-MAY-2001; 2001WO-US017086.

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This invention describes a novel composition comprising an enzyme which contains a heterologous functional domain that provides altered contains a heterologous functional domain that provides altered comprises a functionality in a nucleic acid cleavage assay. The enzyme comprises a 5, conclease, preferably a thermostable 5, nuclease, or a polymerase which is altered in sequence related to a naturally occurring sequence of a colymerase such that it exhibits reduced DNA synthetic activity from that cof the naturally occurring polymerase. Preferably the polymerase is a thermostable polymerase from a Thermus species such as T. aquaticus, T. Clarvage assay and an amino acid sequence that provides an improved substrate binding activity in the nucleic acid cleavage assay and an amino acid sequence that provides improved background specificity in the nucleic acid (a cytochrome cleavage structure comprises a RNA target nucleic acid (a cytochrome cleavage structure comprises a RNA target nucleic acid (a cytochrome comprises an non-target cleavage of the invasive cleavage structure comprises of fluorescence energy transfer or by detecting radioctivity luminescence, which is then detected by detecting radiocativity luminescence, which is then detected by colleavage product. The enzyme is useful for cleaving a nucleic acid which involves exposing a sample (a cell lysate) comprising substrate cleavage product. The enzyme is employed for detecting target DNAs and mutant alleles of genes including genes crown when any other animal or plants that are or may be used. If or her animal or plants that are or may be associated with for the enzyme is employed for may be associated with the colleavage product. The enzyme is employed for may be associated with for the enzyme is employed for may be associated which its colleavage browner and mutant alleles of genes including genes are associated when the partyme is the partyme and mutant a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease or other conditions. In addition, the enzymes may be useful for detecting and identifying strains of microorganisms including bacteria, fungi, protozoa, ciliates and viruses, preferably detecting and
                                                                                                                                                                                                                                                                                                                                                                                                    Composition comprising enzyme which comprises heterologous functional domain that provides altered functionality in nucleic acid cleavage assay, useful for cleaving nucleic acid, and detecting presence of RNA
                                                                                                                                                                                                                                         V, Ma W;
Takova TY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rotozoa, ciliates and viruses, preferably detecting and ing viruses having RNA genomes, such as hepatitis C and human
                                                                                                                                                                                                     Hall JG;
V, Ma to
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0
                                                                                                                                                                                                                Chehak L, Curtis ML, Eis PS,
ski RW, Lukowiak AA, Lyamichev
Schaefer JJ, Skrzypczynski Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.3%; Score 15.2; DB 7; Length 21, 50.0%; Pred. No. 6.6e+03; ive 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 9 A; 3 C; 8 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 95; SEQ ID NO 2144; 1266pp; English.
                                                                                                                                                             (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                  i, Bartholomay CT, Chehak
Kaiser M, Kwiatkowski RW,
nnoz MC, Olson SM, Schaefe
                                                                                                                                                                                                                                                                                            Lyamichev NE, Neri BP;
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Best Local Similarity 50.0%;
Matches 10; Conservative
                                               11-JAN-2001; 2001US-00758282
24-MAY-2001; 2001US-00864426
24-MAY-2001; 2001US-00864636
                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-083110/11.
                                                                                                                                                                                                                                         Ip HS, Kaiser M
Olson-Munoz MC,
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Gaps 20 GTCTCCTTTTGCCAGTTC 1 BP ADI94589/c ID ADI94589 standard; DNA; 22 ADI94589; RESULT 11

Murine IFN-gamma associated probe SEQ ID 2142.

04-NOV-2004 (first entry)

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BP

ADI94590 standard; DNA; 27

AD194590

(first entry)

04-NOV-2004

ADI94590;

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This invention describes a novel composition comprising an enzyme which contains a heterologous functional domain that provides altered to contains a heterologous functional domain that provides altered to contains a heterologous functional domain that provides altered to an unclease, preferably a thermostable 5' nuclease, or a polymerase which is altered in sequence related to a naturally occurring sequence of a polymerase such that it exhibits reduced DNA synthetic activity from that of thermostable polymerase from a Thermus species such as T. aquaticus, T. flavus, T. thermophilus, T. filiformus or T. scotoductus. The enzyme comprises a hereologous functional domain, an amino acid sequence that provides an improved substrate binding activity in the nucleic acid cleavage assay and an amino acid sequence that provides improved cleavage assay and an amino acid sequence that provides improved cleavage structure comprises a RNA target nucleic acid (a cytochrome P550, or cytokine RNA). Cleavage product, which is then detected by detecting radioactivity luminescence, phosphorescence, fluorescence of polarisation or charge. The enzyme is useful for cleavaing a uncleic acid to the enzyme which produces at least one detectable culcavage product. The enzyme is useful for cleavaing a uncleic acid to the enzyme which produces at least one detectable culcavage product. The enzyme is employed for detecting target DNAs and RNAs comprising wild-type and mutant alleles of genes including genes from humans, other animal or plants that are or may be associated with allesses or other conditions. In addition, the enzyme any beatspeciated with allesses or other conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detecting and identifying strains of microorganisms including bacteria, fungi, protozoa, ciliates and viruses, preferably detecting and identifying viruses having RNA genomes, such as hepatitis C and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising enzyme which comprises heterologous functional domain that provides altered functionality in nucleic acid cleavage assay, useful for cleaving nucleic acid, and detecting presence of RNA
functional domain; nucleic acid cleavage assay; nuclease; polymerase;
detection; microorganism; RNA genome; hepatitis C;
human immunodeficiency virus; 88; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                    H, Bartholomay CT, Chehak L, Curtis ML, Bis PS, Kaiser M, Kwiatkowski RW, Lukowiak AA, Lyamichev unoz MC, Olson SM, Schaefer JJ, Skrzypczynski Z, KL, Lyamichev NE, Neri BP;
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                                                                                                                                                                                                                                                                                                                                                                                                (THIR-) THIRD WAVE TECHNOLOGIES INC.
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24-MAY-2001; 2001US-0086426.
24-MAY-2001; 2001US-00864636.
                                                                                                                                                                                                                                    24-MAY-2001; 2001WO-US017086
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                                                                                                                                           WO200190337-A2
                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                  24-MAY-2000;
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Takova TY; Hall JG; V, Ma W;

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63.3%; Score 15.2; DB 7; Length 22; 50.0%; Pred. No. 6.6e+03; ive 7; Mismatches 3; Indels
                                                                  s eucucuccumoeccaecuc 24
                                     10; Conservative
                Best Local Similarity Matches 10; Conserv
     Query Match
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This invention describes a novel composition comprising an enzyme which contains a heterologous functional domain that provides altered to contains a heterologous functional domain that provides altered functionality in a mucleic acid cleavage assay. The enzyme comprises a 5' nuclease, preferably a thermostable 5' nuclease, or a polymerase a 5' contains sequence related to a naturally occurring polymerase which is a contained polymerase from a Thermus species such as T. aquaticus, T. thermophilus, T. filiformus professes and a comprises a heterologous functional domain, an amino acid sequence that provides an improved substrate binding activity in the nucleic acid cleavage assay and an amino acid sequence that provides improved cleavage structure comprises a RNA target nucleic acid (a cytochrome cleavage structure comprises as RNA target nucleic acid (a cytochrome cleavage structure comprises as RNA target nucleic acid (a cytochrome cleavage structure comprises or fluorescence annon-target cleavage product, which is then detected by detecting radioactivity luminescence, phosphorescence fluorescence code action or charge. The enzyme is useful for cleavage aubstrate code which involves exposing a sample (a cell lysate) cone detectable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid to the enzyme which produces at least one detectable cleavage product. The enzyme is employed for detecting target DNAs and RNAs comprising wild-type and mutant alleles of genes including genes from humans, other animal or plants that are or may be associated with disease or other conditions. In addition, the enzymes may be useful for detecting and identifying strains of microorganisms including bacteria, fundi, protozoa, ciliates and viruses, preferably detecting and including and identifying viruses having RNA genomes, such as hepatitis C and human
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Takova TY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition comprising enzyme which comprises heterologous functional domain that provides altered functionality in nucleic acid cleavage assay, useful for cleaving nucleic acid, and detecting presence of RNA
                                                                                                                                                functional domain; nucleic acid cleavage assay; nuclease; polymerase;
detection; microorganism; RNA genome; hepatitis C;
human immunodeficiency virus; 88; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hall JG;
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                                                                                                      Murine IFN-gamma associated probe SEQ ID 2143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 95; SEQ ID NO 2143; 1266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-2000; 2000US-00577304.
11-JAN-2001; 2001US-00758282.
MAY-2001; 2001US-00864426.
24-MAY-2001; 2001US-00864636.
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                                                                                                                                                                                                                                           Mus musculus.
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polarisation or charge. The enzyme is useful for cleaving a nucleic acid
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                                                                                                                                                                                                                              Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel composition comprising an enzyme which contains a heterologous functional domain that provides altered functionality in a nucleic acid cleavage assay. The enzyme comprises a 5 nuclease, preferably a thermostable 5 nuclease, or a polymerase which is altered in sequence related to a naturally occurring sequence of a polymerase such that it exhibits reduced DNA synthetic activity from that of the naturally occurring polymerase. Preferably the polymerase is a thermostable polymerase from a Thermus species such as T. aquaticus, T. flavus, T. thermophilus, T. fillformus or T. scotoductus. The enzyme comprises a heterologous functional domain, an amino acid sequence that provides an improved substrate binding activity in the nucleic acid cleavage assay and an amino acid sequence that provides improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    background specificity in the nucleic acid cleavage assay. The invasive cleavage structure comprises a RNA target nucleic acid (a cytochrome P450, or cytoKine RNA). Cleavage of the invasive cleavage structure generates an non-target cleavage product, which is then detected by detecting fluorescence, mass or fluorescence energy transfer or by detecting radioactivity luminescence, phosphorescence, fluorescence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hall JG;
V, Ma W;
Takova TY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition comprising enzyme which comprises heterologous functional domain that provides altered functionality in nucleic acid cleavage assay, useful for cleaving nucleic acid, and detecting presence of RNA
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                           nuclease; polymerase;
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Lyamichev V
                                        Score 15.2; DB 7; Length 27;
Pred. No. 6.8e+03;
7; Mismatches 3; Indels
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               G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                       functional domain; nucleic acid cleavage assay; detection; microorganism; RNA genome; hepatitis human immunodeficiency virus; ss; probe.
                                                                                                                                                                                                                                                                                                                          Murine IFN-gamma associated probe SEQ ID 2141.
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                                                                                                                            5 GUCUCUCCUTUCGCCACCUC 24
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24-MAY-2001; 2001US-00864426.
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                                                           50.0%;
                                                                                                                                                                                                                           ADI94588 standard; DNA; 28
                                                                                                                                                                                                                                                                                          (first entry)
                                                             Best Local Similarity 50.0
Matches 10; Conservative
               BP; 3 A; 10
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             Sequence 27
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                                             Query Match
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target; substrate; catalyst; modulation; expression; Raf gene; delivery;
szeening; identification; synthesis, deprotection; purification; cancer;
inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
restenosis; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphosphates
which involves exposing a sample (a cell lysate) comprising substrate nucleic acid to the enzyme which produces at least one detectable cleavage product. The enzyme is employed for detecting target DNAs and RNAs comprising wild-type and mutant alleles of genes including genes from humans, other animal or plants that are or may be associated with disease or other conditions. In addition, the enzymes may be useful for detecting and identifying strains of microorganisms including bacteria, fungl, protozoa, ciliates and viruses, preferably detecting and identifying viruses having RNA genomes, such as hepatitis C and human
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A method has been developed for the identification of a nucleic acid
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Burgin A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human C-raf hammerhead ribozyme nucleotide position 220.
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Parry T, Beigelman L, Mcswiggen JA, Karpeisky A,
Thompson J, Workman CT, Beaudry A, Sweedler D;
                                                                                                                                                                                                                 Sequence 28 BP; 3 A; 11 C; 4 G; 10 T; 0 U; 0 Other;
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J, Workman CT, Beaudry A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used as antiviral agents and synthons.
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                                                                                                                                                                                                                                                                                                                                S GUCUCUCCUUUCGCCACCUC 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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97US-0051718P.
97US-0056808P.
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97US-0061324P.
97US-0064866P.
97US-0068212P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV91451 standard; RNA; 29
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                                                                                                                                                                           Immunodeficiency virus.
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19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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comprises: (a) introducing into the system a random library of nucleic acid catalyste (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalysic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of a least part of the SBDs in such systems. Nucleic acid molecules with endomuclease activity and exalytic, activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic ascites and infection. They may also be used to detect genetic drift and muttations in diseased cells and to determine c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-raf. Introduction of suchity, AAV90922 to AAV93877 reperses tability against nuclease and activity. AAV90922 to AAV93877 repersesion of a Raf gene method, specifically for modulating the expression of a Raf gene 

61.7%; Score 14.8; DB 2; Length 29; 47.4%; Pred. No. 1e+04; ive 7; Mismatches 3; Indels Sequence 29 BP; 11 A; 3 C; 9 G; 0 T; 5 U; 1 Other; 6 ucucuccumcaccaccuc 24 Local Similarity 47.4%; les 9; Conservative Query Match

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Gaps

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AAF01081 standard; RNA; 29 (first entry) Hammerhead ribozyme #1072 16-FEB-2001 AAF01081; 

BP

Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.

WO200061729-A2 Homo sapiens

19-OCT-2000

11-APR-2000; 2000WO-US009721

99US-0129390P 12-APR-1999;

(RIBO-) RIBOZYME PHARM INC.

Mcswiggen J; Zwick M, Pavco P, Blatt L,

WPI; 2000-647423/62.

Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin. Claim 32; Page 80; 164pp; English.

The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATI Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoletin, granulocyte colony stimulating factor protein and interferon alpha

Gaps ö 29; Indels Score 14.8; DB 3; Length Pred. No. 1e+04; Seguence 29 BP; 13 A; 2 C; 9 G; 0 T; 4 U; 1 Other; 7; Mismatches 29 TCTCTCTTTCGNCTCATC 11 6 ucucuccunuceccaccuc 24 Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative ž8 요 ઠે

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completed: October 16, 2006, 14:16:00 Search completed: Octobook

OM nucleic

Run on:

Sequence:

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AX649756 Sequence
A24320 LST3 primer
AR010021 Sequence
124749 Sequence 12
BD17716 Method fo
BD187175 Method fo
AX648244 Sequence
AR229112 Sequence
AR229112 Sequence
AR229112 Sequence
AR3137580 Sequence
AR312823 Sequence
AR312823 Sequence
AR349749 Sequence
AR594429 Sequence
AR59425 Sequence
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                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 24)
Johnson, E.M. and Bergemann, A.D.
Cloning and expression of FUR protein
Patent: US 5756684-A 20 26-MAY-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      24 bp | Sequence 20 from patent US 5756684. AR010008
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 38 from patent US 5756684.
AR010025 GI:3968830
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1 (bases 1 to 24)
Johnson, E.M. and Bergemann, A.D.
                                                                AX648244
BD268715
CQ764854
AR229112
AR21375
AR312623
AR337580
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AR014743 Sequence
AR014763 Sequence
AR034760 Sequence
124740 Sequence 3
124752 Sequence 15
BD55215 Sequence
AR072296 Sequence
AR072296 Sequence
126407 Sequence 38
IS847 Sequence 38
AX649751 Sequence
AX649752 Sequence
                                                               October 16, 2006, 13:57:30 ; Search time 590.797 Seconds (without alignments) 2597.742 Million cell updates/sec
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AX649754 Sequence
AX649755 Sequence
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            GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Maximum Match 100%
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Searched:

PAT 04-DEC-1998

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124740.1 GI:1604610
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1 (bases 1 to 24)
Johnson, E.M. and Bergemann, A.D.
Monoclonal antibodies to the pur protein
Patent: US 5869622-A 20 09-FEB-1999;
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Johnson, E.W. and Bergemann, A.D.
Monoclonal antibodies to the pur protein
Patent: US 5869622-A 38 09-FEB-1999;
Location/Qualifiers
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and expression of PUR protein US 575684-A 38 26-MAY-1998; Location/Qualifiers
                                                                                                                       7; Mismatches
                                                 /organism="unknown"
/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Sequence 38 from patent US 5869622.
AR034760.1 GI:5950365
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/wol_type="unassigned DNA"
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Seguence 20 from patent US 5869622.
AR034743
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AR034760
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Regulation of repressor genes using nucleic acid molecules. BD253279
BD253279. GI:33063049
JP 2002541795-A/1072.
PAT 07-0CT-1996
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unclassified sequences.
1 (bases 1 to 2 wick, M., Pavco, P. and Mcswiggen, J.
Regulation of repressor genes using nucleic acid molecules
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50.0%; Pred. No. 1.9e+04;
tive 7; Mismatches 4;
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Johnson, E.M. and Bergmann, A.D.
Cloning and expression of pur protein
Patent: US 5545551-A 3 13-AUG-1996;
Location/Qualifiers
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1 (bases 1 to 24)
Johnson, E.M. and Bergmann, A.D.
Cloning and expression of pur protein
Patent: US 554551-A 15 13-AUG-1996;
Location/Qualifiers
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124752
124752.1 GI:1604622
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124740 24 bp
Sequence 3 from patent US 5545551.
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/organism="unknown"
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                                        DESCRIPTION OF SERVEY OF S
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Sucov.H.M., Evans,R.M. and Umesono,K.
Sucov.H.M., Evans,R.M. and ussays employing same Response element compositions and assays employing same Patent: US 492137-A 16 10-DEC-2002;
The Salk Institute for Biological Studies; La Jolla, CA Location/Qualifiers
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Location/Qualifiers
Patent: JP 2002541795-A 1072 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
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Sequence 99 from patent US 5948611.
AR072296.1 GI:9999060
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Sequence 16 from patent US 6492137.
AR265215.1 GI:29693642
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/mol_type="genomic DNA"
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(C12N5/00,C12R1:91)
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23 CTGTCCTTTCGTCACCTC
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AR265215/c
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1 (bases 1 to 18)
Prockop, D.J., Ala-Kokko, L., Williams, C.J., Ritvaniemi, P.,
Baldwin, C., Hopkinson, I. and Ahmad, N. Nina.
Primers and methods for detecting mutations in the procollagen II
gene (COL2A1) that indicate a genetic predisposition for a
COL2A1-associated disease
Patent: US 5948611-A 99 07-SEP-1999;
Location/Qualifiers
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Prockop, D.J., Ala-Kokko, L. and Ritvaniemi, P.
Primers and methods for detecting mutations in the procollagen II
gene that indicate a genetic predisposition for osteoarthritis
Patent: US 5558988-A 99 24-5EP-1996;
Location/Qualifiers
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62.5%; Pred. No. 6.5e+04;
ive 5; Mismatches 1;
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1 (bases 1 to 21)
Watanabe, K. A., Ren, W.-Y. and Weil, R.
Complementary DNA and toxins
Patent: US 5571937-A 38 05-NOV-1996;
Location/Qualifiers
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Sequence 38 from patent US 5571937.
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Sequence 99 from patent US 5558988.
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                                                                 AX649751.1 GI:29152569
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Matches 10; Conservative
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RESULT 14
AX649751/c
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AX649752/c
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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                          59.2%; Score 14.2; DB 2; Length 21; 36.8%; Pred. No. 8.1e+04;
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Patent: EP 1273660-A 1590 08-JAN-2003;
Aeomica, Inc. (US)
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59.2%; Score 14.2; DB 2;
Best Local Similarity 36.8%; Pred. No. 8.1e+04;
Matches 7; Conservative 9; Mismatches 3;
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Watanabe,K.A., Ren,W.-Y. and Weil,R.
Complementary DNA and toxins
Patent: US 5652350-A 38 29-JUL-1997;
Location/Qualifiers
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Sequence 1590 from Patent EP1273660.
AX649750. GI:29152568
                                                     9; Mismatches
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Sequence 38 from patent US 5652350.
158747 GI:2477985
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Location/Qualifiers
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                                       Best Local Similarity 36.8
Matches 7; Conservative
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Best Local Similarity 52.6
Matches 10; Conservative
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Patent: EP 1273660-A 1591 08-JAN-2003;
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Patent: EP 1273660-A 1592 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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52.6%; Pred. No. 8.2e+04;
iive 6; Mismatches 3;
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Sequence 1591 from Patent EP1273660.
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Location/Qualifiers
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AZ775852 2M0009001
BQ586604 E012388-0
AI673609 wer6605.x
CL983097 GC0336 T1
AZ604126 1M0423013
CA850924 D08B11 D2
AZ34025 1M0054A13
AZ34058 1M0054A13
AZ34561 1M0054A13
AZ514958 1M0054A13
AZ514958 1M0054A13
AZ514958 1M0294A14
AZ5158310 Drosophil
AZ475883 1M0294J14
AZ475881 Drosophil
AZ475881 Drosophil
AZ475881 0M0296G18
AI83010 ub92e02.r
AZ780850 2M0018A02
AZ628692 2M0105N15
AZ432080 1M0217024
                                                                                   October 16, 2006, 14:04:23 ; Search time 1032.18 Seconds (without alignments) 1300.222 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                 48236798 seqs, 27959665780 residues
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ALGASGO9
CL983C09
CL983C097
AZGO4126
CA85C024
AZ34C28
AZ34C58
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Maximum Match 100%
Listing first 45 summaries
                                                        OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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24
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Query
Match Length DB
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                                                                                                                                             Title:
Perfect score:
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13.4
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AI539240 AZ454352 AI183010

AZ780850 AZ828692 AZ432080

21 22 23 24 2 25 2 25 2 27 2 27 2 31 2 31 2 31 2 31 2 31 3 31 3 31 3 31 3 31 4 41 4 42 4 41 4 42 4 41 4 42 4 43 4 44 4 45 4 45 4 45 4 45 4 46 4 47 4 45 4 45 8 6 000 8 6 000 8 7 000 8 7 000 8 8 000 8 000	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	11. 4 4 111. 2 1	058822 078852	11.4 47.5 28 1 AII18 11.4 47.5 28 11 AZ24 11.4 47.5 28 11 AZ24 11.4 47.5 29 11 AZ24 11.2 46.7 29 13 CZ24 11.2 46.7 21 14 AG28 11.2 46.7 29 12 BZSS 11.2 46.7 27 11 AZ87 11 45.8 22 1 AU014 11 45.8 22 1 AZ87 11 45.8 22 1 A	28 1 1 2 2 8 1 1 1 2 2 8 1 1 1 2 2 8 1 1 1 2 2 8 1 1 1 2 2 2 1 1 1 4 2 1 1 1 1 4 2 1 1 1 1	AZ3, AZ3, AZ3, AZ11, AZ11, AZ1, AZ1, AZ2, AZ2, AZ2, AZ2, AZ2, AZ2, AZ2, AZ2	AII18404 AZ342196 AZ342196 AZ345296 AZ345299 CZ477219 CZ477219 CZ477219 CZ477219 CZ477219 CZ775612 CZ1692271 AZ416143 AZ1614183 CZ175615 CZ175615 CZ175615 CZ175615 AZ16143 AZ1614183 AZ242905 AZ16285 AZ376285 AZ	8404 A1219 65504 772219 772219 772219 772219 772219 772219 77242 60241 8412 8412 8412 75134 A1100 A110		1118404 u 2342196 (2342196 17247219 17247219 17247219 17247219 17247219 17247219 17247219 172618 172	A1118404 ue36c02.x A2342196 in0075F07 A1479131 T. burcei A2345594 in0080016 C24772219 d01414-5p C2477542 d11088-5p CN750241 ApDT-VIII AG189071 Pan trog1 AG202804 Pan trog1 AG202804 Pan trog1 AG202805 Pan trog1 AG20280607.x AG2028060608 AG20280608 AG20280608 AG20280608 AG20280608 AG20280608 AG20280608 AG20280608 AG20280608 AG202808 AG
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Gaps

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EST 18-DEC-1999

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Ouble-stranded CDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT13 vector. Library went through one round of normalization. Tissue samples provided by Dr. Brian Dieckgraefe (Washington University, dieck@im.wustl.edu); colonic mucosa represents a range of disease involvement from moderate to severe Crohn's disease; samples include both perforating (fistulas) and non-perforating samples. Library constructed by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 28)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

Yational Cancer Institute, Cancer Genome Anatomy Project (CGAP); Thmor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
This clone is available royalty-free through LLNL; contact the
This Conne is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 850 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              55.8%; Score 13.4; DB 3; Length 26; 47.8%; Pred. No. 3.3e+05; ive 6; Mismatches 6; Indels
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/organism="Homo sapiens"
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Best Local Similarity 47.8
Matches 11; Conservative
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (bases 1 to 26)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., and Radelof, M., Etahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 26 Std Error: 0.00
Plate: 12 row: E column: 21
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
Location/Qualifiers
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/db_xxef="taxon:161934"
/clone="024-012-E21"
/tlsue_type="leaf"
/lab_host="EMDH108"
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EST.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gil #732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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D08Bll_D23_04.abl cDNA Peking library 2, 4 day SCN3 Glycine max
CA850924
                                                                                                                                                                                                                                                                                                                                                                                 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Whose whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: (
Plate: 0423 row: O column: 13
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. 30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGCIM0423013"
                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                       Mus musculus (house mouse)
Mus musculus
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Best Local Similarity 40.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                  CL983097 21-SEP-2004 GC0336 TIGEM gene trap library Mus musculus cDNA clone 10662.60,
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Sequence tag generated by 5' RACE of total RNA from gene trap ES
Sequence tag generated by 5' RACE of total RNA from gene trap ES
Genell line. ES cell lines harboring insertion mutation of target
gene are available upon request from TIGEM. Annotation information
available from TIGEM
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                           Length 28;
                                                                                           5; Indels
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/cell_line="E14"
/clone_lib="TibEM gene trap library"
/note="Vector: pFLIP1"
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Tel: +390816132205
Fax: +390815790919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tagging genes with cassette-exchange sites
Nucleic Acids Res. 33 (4), e44 (2005)
                                             DB 1;
                                           54.2%; Score 13; DB 1;
38.1%; Pred. No. 5e+05;
iive 8; Mismatches
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clone="10662.60"
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/strain="129 ola"
                                                                                                                                      1 UAUUGUCUCCCUUUCGCCAC 21
                                                                                                                                                                B TCTGTTCTTTTTCTCCAC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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AZ604126.1 GI:11726316
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                     Conservative
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/lab host-wate.
/lab host-wate.
/lab host-wate.
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_wetor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose get a 9.5 to
10.5 kb range using preparative agarose get of a 9.5 to
cf pWD42 (gil 4732114 gb | AF129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukeryota; Metazoa; Chordata; Craniata; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
E (bases 1 to 23)
Sciurognathi; Muroidea; Murinae; Mus.
E (bases 1 to 23)
Sunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von
Dlasmid inserts
L Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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1M0054A13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic CODE UUGCIM0054A13 R, genomic survey sequence.
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                           0.00
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0072 row: C column: 20
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
High quality sequence
                                                                                                                                                                                                              /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC1M0072C20"
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Alkharouf,N., Khan,R. and Matthews,B.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Genome 47 (2), 380-388 (2004)
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                                                                                                       Eukaryona; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                      Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
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Dunn, D., Aoyagi, A., Barber, M., Meenen, E., Pedersen, T., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niderhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Roots"
/dev stage="Seedlings"
/dow stage="seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
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University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
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/cultivar="Peking"
/db_xref="taxon:3847"
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Mus musculus
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     CA850924.1 GI:33387717
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504 5728
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Fax: 801 585 7177
                                                                                      Glycine max
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Fax: 301
                                                                                                                                                                                                Glycine.
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Similarity 50.0%; 6; Conservative 6
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11 TATTGTCTCTCC 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucjectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XII0-GG14 (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ514958 1005-00T-2000 1M0054A13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0054A13 F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                          /clome_lib="Mouse 10kb plasmid UUGCiM library"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                  /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Pred. No. 1.4e+06;
6; Mismatches 0; Indels
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0054 row: A column: 13
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Class: plasmid ends
High quality sequence stop: 23.
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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GC0348 TIGEM gene trap library Mus musculus cDNA clone 10863.13,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glifes, Rodentia,
Sciurognathi, Muroidea, Murinae, Mus.
1 (bases 1 to 27)
Cobellis, G., Nicolaus, G., Iovino, M., Romito, A., Marra, E.,
Barbarisi, M., Sardiello, M., Di Giorgio, F.P., Iovino, N., Zollo, M.,
Ballabio, A. and Cortese, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone l1b="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tagging genes with cassette-exchange sites Nucleic Acids Res. 33 (4), e44 (2005) 15741177
Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Inscrt Length: 10000 Std Error: 0.00

Plate: 0054 row: A column: 13
                                                                                                                                                                     Seg primer: CGTTGTAAAACGACGGCAGT
Class: plaamid ends
High quality sequence stop: 23.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
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CL983109
CL983109.1 GI:52420701
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AZ475883 21 bp DNA linear GSS 04-OCT-2000 lM0294J14F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0294J14 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                          DMES45811 28 bp DNA linear GSS 24-FEB-2003 Drosophila melanogaster flanking sequence of RS P element insertion P{RS}CB-6297-3, clone library P{RS3}, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-FEB-2003) Ryder E.J., Department of Genetics, University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM The insertion point of the Pelement is before base 1 of the sequence. Further information about this P element insertion line can be found at http://www.flyseq.org.uk and http://www.drosdel.org.uk.
the site of insertion. Details of the protocols used car
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mapping of RS P element insertions in Drosophila melanogaster for
the DrosDel second generation deficiency kit
Unpublished
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                                                                                                                                         Gape
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                         Length 28;
                                                                                                                                         5; Indels
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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_kref="taxon:7227"
                                                                                           Score 12; DB 11;
Pred. No. 1.4e+06;
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40.0%; Pred. No. 1...
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
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/clone_lib="P{RS3}"
/note="read=5' end"
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AJ545811.1 GI:28553693
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25 CTCTCTTCGCCAC 11
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1 (bases I to 28)

2 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Joseke, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

L Unpublished (2001)

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752
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                   Email: coballis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES
Sequence tag generated by 5' RACE of total RNA from gene trap ES
Gene are available upon request from TIGEM. Annotation information
available from TIGEM
Class: Gene Trap.
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/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is single pass sequence recovered from the left border of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 50.0%; Score 12; DB 13; Length 27; I Similarity 55.0%; Pred. No. 1.40+06; 11; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                    /cell_type="Embryonic stem cell"
/cell_line="Ell"
/clone lib="TIGEM gene trap library"
/note="Vector: pFLIP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="10863.13"
                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="129 ola"
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                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: TDNA tagged
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Matches 11; Conserv
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Location/Qualifiers
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                      GI:4453375
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                                                                      Homo sapiens (human)
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Best Local Similarity 44.4
Matches 8; Conservative
                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xili0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                     Journ, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacren, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Weiss University of Utah Genome Center University of Utah Genome Center University of Utah R. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIS39240 25 bp mRNA linear EST 13-MAY-1999 tp64b08.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2204055 3' similar to TR:Q40726 Q40726 DNA BINDING PROTEIN ;, mRNA sequence.
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                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia;
Sciurognathi, Muroidea, Muridae, Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XLI0-Gold, Tl-resistant, F-"
/clone_lib="Mouse_lokb plasmid UTGC1M library"
/note="Vector: FWP42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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48.3%; Score 11.6; DB 11; Length 21;
Best Local Similarity 44.4%; Pred. No. 2e+06;
Matches 8; Conservative 6; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0294 row: J column: 14
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 21.
Location/Qualifiers
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/clone="UUGC1M0294J14"
                                          Mus musculus (house mouse)
  AZ475883.1 GI:10634008
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
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Email: cgapbe-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ454352 1085 04-OCT-200 DNA linear GSS 04-OCT-200 DNA linear GSS 04-OCT-200 UMO256G18F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0256G18 F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                    Hominidae, Homo.

1 (bases 1 to 25)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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/tissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
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Pred. No. 2e+06;
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                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
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plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Unpublished (2000)

COMMENT Unpublished (2000)

Examile diamorgenetical Polymers Research Bldg., 20 S. 2010 E., SLC, UT 84.12, USA

Tel. 801 585 5706

Fax: 801 585 717

Email: diamorgenetics.utah.edu
Insert Leargh: lordon Std Error: 0.00

Plate: 0256 row: G column: 18

Seq primer: CGTTGTAAAACGACGCCAGT

Class: plasmid ends stop: 26.

FEATURES

High quality sequence stop: 26.

Anganiam="Mus musculus"

Amile type="genomic DNA"

Amile type="genomic DNA"

Amile type="genomic DNA"

Amile type="genomic DNA"

Amile host="E. Coli strain XL10-Gold, Tl-resistant, P-"

Alab host="E. Colis s
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Query Match 48.3%; Score 11.6; DB 11; Length 26; Best Local Similarity 50.0%; Pred. No. 2.1e+06; Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps

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7 CUCUCCUUUCGCCACCUC 24 |:|:||::| | ||:| 6 CTCTCCTCTCCTC 23

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Search completed: October 16, 2006, 15:51:29 Job time : 1035.18 secs

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10, Appl
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                                                                                          ; Search time 55.5789 Seconds (without alignments) 807.979 Million cell updates/sec
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1: /EWC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
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               5.1.9
Biocceleration Ltd.
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US-08-048-421-20

US-08-486-421-38

US-08-486-809-38

US-08-486-809-38

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US-08-136-134

US-08-118-408-10

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US-09-118-408-10

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US-09-118-408-10

US-09-118-408-10
                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                 1403666 segs, 935554401 residues
              GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    nucleic search, using sw model
                                                                                             October 16, 2006, 14:11:03
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 30
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                        Scoring table:
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13.8
13.8
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Maximum DB
                                                                                                                                                                              Sequence:
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                                                                                             Run on:
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Sequence 3360, Appl Sequence 10, Appl Sequence 64399, A Sequence 64399, A Sequence 1100, Appl Sequence 100, Appl Sequence 56, Appl Sequence 57, Appl Sequence 57, Appl Sequence 56, Appl Sequence 56, Appl Sequence 56, Appl Sequence 57, Appl Sequence 365, Appl Sequence 365, Appl Sequence 1417, A Sequence 14417, A Sequence 14417, A Sequence 14418, A Sequence 14419, Sequence 117149, Sequence 117149,		Protein	h 24; .ls 0; Gaps 0;
20 3 US-09-198-452A-3360 20 3 US-09-506-852-10 25 3 US-09-396-196G-64399 25 3 US-09-396-196G-119671 17 2 US-07-977-284A-100 24 3 US-08-445-463B-50 24 3 US-08-445-463B-57 24 3 US-08-445-464C-56 24 3 US-08-445-464C-56 24 3 US-08-44-857D-57 24 3 US-08-44-857D-57 24 7 PCT-US94-03437-57 25 3 US-09-544-39BB-365 25 3 US-09-396-196G-14428 25 3 US-09-396-196G-14428 25 3 US-09-396-196G-14428 25 3 US-09-396-196G-57430 25 3 US-09-396-196G-57430 26 3 US-09-396-196G-57430	ALIGNMENTS	rd M.  drew D.  ing And Expression Of PUR monds  trible  OS/MS-DOS  ease #1.0, Version #1.25  //08/014,943A  92  in 6923-033  friron:  0,742  in 6923-033  friron:  3:	65.0%; Score 15.6; DB 2; Length 50.0%; Pred. No. 6.40+02; tive 7; Mismatches 4; Indel.
C 25 13.8 57.5 C 2 24 13.8 57.5 C 2 26 13.8 57.5 C 2 26 13.8 57.5 C 2 2 2 13.8 57.5 C 2 2 2 13.8 57.5 C 2 2 3 1 13.4 55.8 8 6 2 3 2 13.4 55.8 8 6 2 3 2 13.4 55.8 8 6 2 3 2 13.4 55.8 8 6 2 3 2 13.4 55.8 8 6 2 3 2 13.4 55.8 8 6 2 3 2 13.4 55.8 8 6 2 3 2 13.4 55.8 8 6 2 3 2 13.4 55.8 8 6 2 3 2 13.4 55.8 8 6 2 2 3 2 13.4 55.8 8 6 2 2 3 2 4 2 13.4 55.8 8 6 2 2 3 2 4 2 13.4 55.8 8 6 2 2 3 2 4 2 13.4 55.8 8 6 2 2 3 3 3 3 4 55.8 8 6 2 3 3 4 55.8 8 6 2 3 3 3 3 4 55.8 8 6 2 3 3 4 55.8 8 6 2 3 3 3 4 55.8 8 6 2 3 3 3 4 55.8 8 6 2 3 3 3 4 55.8 8 6 2 3 3 3 4 55.8 8 6 2 3 3 3 3 4 55.8 8 6 2 3 3 3 3 4 55.8 8 6 2 3 3 3 3 4 55.8 8 6 2 3 3 3 3 4 55.8 8 6 2 3 3 3 3 4 55.8 8 6 2 3 3 3 3 4 55.8 8 6 2 3 3 3 3 4 55.8 8 6 2 3 3 3 3 4 55.8 8 6 2 3 3 3 3 3 4 55.8 8 6 2 3 3 3 3 3 4 55.8 8 6 2 3 3 3 3 3 4 55.8 8 6 2 3 3 3 3 3 4 55.8 8 6 2 3 3 3 3 3 3 3 3 4 55.8 8 6 2 3 3 3 3 3 3 3 4 55.8 8 6 2 3 3 3 3 3 3 3 3 4 55.8 8 6 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3		RESULT 1 US-08-014-943A-3/C iSequence 3, Application US/08014943A iSequence 3, Application US/08014943A iSequence 3, Application US/08014943A iSequence 3, Application US/08014943A iSequence 3, Application iSTATE: Bergemann, Andrew D. iTILE OF INVENTION: Cloning And NUMBER OF SEQUENCE: 26 CORRESPONDENCE ADDRESS: ADDRESSER: Pennie & Edmonds STREET: New York COUNTRY: U.S.A. ZIP: 10036-2711 COMPUTER: New York COMPUTER: New York COMPUTER: New York COMPUTER: DEADS. ISPENION OF SEQUENCE: OF SEGUENCE COMPUTER: 18M PC COMPATION MEDIUM TYPE: Floppy disk COMPUTER: 18M PC COMPATION MEDIUM TYPE: Ploppy disk COMPUTER: 18M PC COMPATION INTELENT APPLICATION NUMBER: US/08/014, FILING DATE: 0.2) FEB) 1992 CLASSIFICATION NUMBER: 6923- TELECHNOMICATION N	Query M Best Lo Matches

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GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
STATE: 1036-2711
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.0%; Score 15.6; DB 2; Length 24; Best Local Similarity 50.0%; Pred. No. 6.4e+02; Matches 11; Conservative 7; Mismatches 4; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,421
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION 1995
ATFORNEY/AGENT INPORMATION:
NAME: COLUZZ, Laura B, 742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,421
FILING DATE: 07-JUN-1995
CLASSIFICATION 435
PRIOR APPLICATION 198ER: US/08/470,911
APPLICATION NUMBER: US/08/470,911
APPLICATION NUMBER: US/08/470,911
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
RESERENCE/DOCKET NUMBER: 30,742
RESERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
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Patent No. 5672479
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 869-9741/8864
TELEX: 6644 PENNIE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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TELEX: 66141 PENNIE
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WS-048-014-943A-15

Sequence 15, Application US/08014943A

Patent No. 554551

GENERAL INFORMATION:

APPLICANT: Johnson, Edward M.

APPLICANT: Bargemann, Andrew D.

TITLE OF INVENTION: Cloning And Expression Of PUR Protein NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

COMPUTER: New York

COMPUTER: New York

COMPUTER: Patentin Release #1.0, Version #1.25

COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/014,943A

FILING DATE: 02)FEB11992

CLASSIFTCATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: COTUZZI, LBUTA A.

RECISTRATION NUMBER: 6923-033

TELEFAX: 212 869-8864/9741

TELEFAX: 212 869-8864/9741

TELEFAX: 212 869-8864/9741

TELEFAX: APPLICATION FOR SEQ ID NO: 15: SEQUENCE CLARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDENDESS: Angles
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Patent No. 5672479
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                3 UNGUCUCUCCUTUCGCCACCUC 24
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                                          23 TTTCTCCCTCCACCAC 2
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 50.0%
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COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
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STATE: New York
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US-08-486-421-20/c
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MOLECULE TYPE: DNA
      GENERAL INFORMATION:
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STRANDEDNESS:
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                                                                                                                                                                                        Length 24;
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Patent No. 5756684
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
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COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,911
FILING DATE: 06-UUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
RESPERENCE/DOCKET UMBER: 30,742
REDEMONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEFAX: (212) 8664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.0%; Score 15.6; DB 2; Best Local Similarity 50.0%; Pred. No. 6.4e+02; Matches 11; Conservative 7; Mismatches 4;
                                                                                                                                                                                     Query Match 65.0%; Score 15.6; DB 2; Best Local Similarity 50.0%; Pred. No. 6.4e+02; Matches 11; Conservative 7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                2 TTTTCTCTCCCTCCACCTC 23
                                                                                                                                                                                                                                                                        3 UNGUCUCUCCUUUCGCCACCUC 24
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Patent No. 5756684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1155 A. CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-08-470-911-20/c
                                                                                                                                              US-08-486-421-38
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APPLICATI' COHESON EASTERN H.

APPLICATI' BESTGERAIN ANDREW D.

NUMBERS OF SEGURICATE: 51

CORRESSORMER ANDRESS: 51

CONSTRUCT IN STATE OF THE AMERICAN ST
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Query Match 65.0%; Score 15.6; DB 2; Length 24; Best Local Similarity 50.0%; Pred. No. 6.4e+02; Matches 11; Conservative 7; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                       3 ungueucucucuuceccaccuc 24
                                                                                                                                                                    2 TTTCTCTCCTCCACCTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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| Detern No. Se65622 | Detern No. Se65622 | Detern No. Se65622 | Detern No. Se65622 | Detern No. Se65622 | Detern No. Se65622 | Detern No. Se65622 | Detern No. Se65622 | Detern No. Se66622 | Detern No. Se6662 | Detern No. Se6622 | Detern No. Se66222 | Detern No. Se6622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.0%; Score 15.6; DB 2; Length 24; 50.0%; Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
                                                                                            NAME: COLUZI, LAURA A.
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 6923-053
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPKA: (212) 790-9090
TELEKA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDENESS: single
         APPLICATION NUMBER: US 08/470,911
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 UNGUCUCCUTUCGCCACCUC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 TTTTCTCTCCTCCACCACCTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: DNA (genomic) US-08-486-809-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: DNA
US-08-486-809-38
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US-07-672-530C-16/C

US-07-672-530C-16/C

Sequence 16, Application US/07672530C

Patent No. 6492137

GENERAL INFORMATION:
APPLICANT: SUCOV, HERY M

APPLICANT: UNESONO, KAZUHIKO
TILLE REFERENCE: 088802/1552

CURRENT APPLICANT: UNBERN: US/07/672,530C

CURRENT APPLICATION NUMBER: US/07/672,530C

CURRENT APPLICATION NUMBER: 07/438,757

PRIOR APPLICATION NUMBER: 07/438,757

WINDER OF SEQ ID NOS: 51

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 16

LENTH: 29

LENTH: 29
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Waehburn, Kurtz, Mackiewicz & No. 5558988rl8
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Patent No. 5558988

GRNERAL INFORMATION:

APPLICANT: Ala-Kokko, Leena

APPLICANT: Ala-Kokko, Leena

APPLICANT: Ala-Kokko, Leena

APPLICANT: Baldwin, Clinton

APPLICANT: Baldwin, Clinton

APPLICANT: Hopkinson, lan

APPLICANT: Ahmad, Nilofer Nina

TITLE OF INVENTION: METHODS OF DETECTING A GENETIC

TITLE OF INVENTION: PRESISPOSITION FOR OSTEOARTHRITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide, M2
US-07-672-530C-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 61.7%; Score 14.8; DB 3;
Best Local Similarity 55.6%; Pred. No. 1.5e+03;
Matches 10; Conservative 6; Mismatches 2;
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Gaps

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1; Indels

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59.2%; Score 14.2; DB 2; Length 21; 36.8%; Pred. No. 2.7e+03;
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APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Weil, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESORNENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
                                                                                                                                                                                               Query Match 60.0%; Score 14.4; DB 2; Best Local Similarity 62.5%; Pred. No. 2.1e+03; Matches 10; Conservative 5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,664
FILING DATE: May 12, 1994
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38, Application US/08242664
Patent No. 5571937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPERENCE/DOCKET NUMBER: 4468
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza CIIY: New York STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 UAUUGUCUCUCCUUUCGCC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS: LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 TTTTATCTCTCCTTTCTCC
                                                                                                                                                                                                                                                                                                                            3 CTCCTTTCCCCACCTC 18
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Best Local Similarity 36.8%
The Conservative
                           LENGTH: 18
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
NO NATI-SENSE: NO US-08-256-426B-99
          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-242-664-38/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-08-484-138-38/c
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%; Score 14.4; DB 2; Length 18; 62.5%; Pred. No. 2.1e+03; ive 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ala-Kokko, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Ala-Kokko, Charlene J.
APPLICANT: Ritvaniemi, Pertii
APPLICANT: Baldwin, Clinton
APPLICANT: Hopkinson, lan
APPLICANT: Hopkinson, lan
APPLICANT: Hopkinson, lan
APPLICANT: Hopkinson, lan
APPLICANT: Mand, Nilofer Nina
TITLE OF INVENTION: Methods of Detecting A Genetic
NUMBER OF SEQUENCES: 293
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Mashburn Kurtz Mackiewicz & No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: DESCRITE, 3.5 INCH
COMPUTER: DESCRITE, 3.5 INCH
COMPUTER: WINDERFERET
SOFTWARE: WORDERFERET
CONFINCATION DATA:
APPLICATION NUMBER: US/08/256,426B
FILING DATE: 03-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10964
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,284
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: MAIK DELUCA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark:
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0697
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1082
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-256-426B-99
Sequence 99, Application US/08256426B
Patent No. 5948611
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TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 CUCCUTUCGCCACCUC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CTCCTTTCCCCACCTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.0°
Best Local Similarity 62.5°
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                LENGTH: 18
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-977-284A-99
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Gaps

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GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: Cloning And Expression Of PUR Protein
INUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: DALANT: PS-DOS/MS-DOS
COMPUTER: DALANT: PS-DOS/MS-DOS
COMPUTER: DALANT: DALANT: PS-DOS/MS-DOS
COMPUTER: DALANT: DAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.2%; Score 14.2; DB 7; Length 21; Best Local Similarity 36.8%; Pred. No. 2.7e+03; Matches 7; Conservative 9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 24;
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 02/08/014,943A
FILING DATE: 02/08/014,943A
FILING DATE: 02/08/014,943A
FILING DATE: 02/08/014,943A
ATTONNEY/AGENT INFORMATION:
NAME: CCTUZZi, LBUEA A.
REGISTRATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 6923-033
TELEFAKICE/POCKET NUMBER: 6923-033
TELEFAK: 212 669-8864/9741
TELEFAK: 212 869-8864/9741
TELEF SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: NUCleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.3%; Score 14; DB 2; 40.9%; Pred. No. 3.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                         44683-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-014-943A-12/c
; Sequence 12, Application US/08014943A
; Patent No. 5545551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 UNGUCUCUCCUUNCGCCACCUC 24
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4468
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFRAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 UAUUGUCUCCCUTUCGCC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 TTTATCTCCTTTCTCC 1
                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) PCT-US95-06379-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
Matches 9; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-014-943A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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; Sequence 38, Application PC/TUS9506379
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyolchi A.
APPLICANT: Ren, Wu-Yun
; APPLICANT: Ren, Wu-Yun
; TITLE OF INVENTION: Complementary DNA and Toxins
; CORRESPONDENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
   APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Mu-Yun
APPLICANT: Weil, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER:
APPLICATION NUMBER:
FLILING DATE: JUNE 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG
TELEPHONE: 212-977-9550
TELEPHONE: 212-977-9550
TELEPHONE: 212-64-0525
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
STRANDEDNESS: double
STRANDEDNESS: DANA (COLOMIC)
MATERIAL DANA (COLOMIC)
STRANDEDNESS: DANA (COLOMIC)
MATERIAL DANA (COLOMIC)
MATERIAL DANA (COLOMIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06379
FILING DATE: May 13, 1994
                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 35 inch 1.44Mb
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 UAUUGUCUCUCCUUUCGCC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 59.2
Best Local Similarity 36.8
Matches 7; Conservative
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1: New York
TRY: U.S.A.
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Search completed: October 16, 2006, 14:47:14 Job time : 56.5789 secs

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"US-10-719-900-980988
; Sequence 980988, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial
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1: KBMC Celerra_SIDS3/prodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /BMC_Celerra_SIDS3/prodata/2/pubpna/USO8_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/prodata/2/pubpna/USO9A_PUBCOMB.seq:*
4: KBMC_Celerra_SIDS3/prodata/2/pubpna/USO9B_PUBCOMB.seq:*
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6: /EMC_Celerra_SIDS3/prodata/2/pubpna/USO0C_PUBCOMB.seq:*
7: KBMC_Celerra_SIDS3/prodata/2/pubpna/USIOR_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/prodata/2/pubpna/USIOR_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/prodata/2/pubpna/USIOR_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/prodata/2/pubpna/USIOR_PUBCOMB.seq:*
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16: /EMC_Celerra_SIDS3/prodata/2/pubpna/USIIA_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 336045
                                                                                           October 16, 2006, 14:16:09; Search time 337.985 Seconds (without alignments) 872.534 Million cell updates/sec
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            GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-719-900-980988

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US-10-956-157-88877

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US-10-956-157-88877

US-11-060-756-4778

US-11-136-527-276878

US-10-131-957-276878

US-10-136-527-276878

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US-10-136-527-276878

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US-10-956-157-21637
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Sequence 2144, Ap Sequence 2144, Ap Sequence 2142, Ap Sequence 2142, Ap Sequence 2142, Ap Sequence 2143, Ap Sequence 2141, Ap Sequence 2141, Ap Sequence 2141, Ap Sequence 2141, Ap Sequence 661177, Sequence 661177, Sequence 42356, A Sequence 43354, A Sequence 43359, A Sequence 88872, A Sequence 868872, A Sequence 88872, A Sequence 868872, A Sequence 8688
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Fublication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Myeth

APPLICANT: Myeth

TITLE OF INVERTION Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AM101086)

CURRENT FILING DATE: 2005-05-25

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR APPLICATION NUMBER: US 60/574,294

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: PatentIn version 3.2

LENGTH: 25
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                                                                                                                                                                                      US-09-864-626A-2142

US-09-864-636A-2143

US-09-864-636A-2143

US-09-864-636A-2143

US-10-084-839-2141

US-10-084-839-2141

US-10-084-839-2141

US-10-084-426A-2141

US-10-084-426A-2141

US-10-084-426A-2141

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US-10-956-157-43354

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Sequence 88877, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: HUANN OSTEDARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319905

SOFTWARE: Patentin version 3.2

SEQ ID NO 88877

LENGTH: 25
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Sequence 47774, Application US/11060756

GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE REPRESENCE: AMIJO1083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEC ID NOS: 303284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      William Martin
Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
Target Genes
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45.8%; Pred. No. 4.5e+03;
tive 8; Mismatches 5;
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66.7%; Score 16; DB 13;

Best Local Similarity 45.8%; Pred. No. 4.5e+03;

Matches 11; Conservative 8; Mismatches 5.
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Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Worth
APPLICANT: Mounts, William Martin
TITLE OF INVERTION: Nucleic Acid Arrays
TITLE OF INVERTION: Target Genes
                                           2 TATTGTCTCTCATAGCACCACATC 25
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SEQ ID NO 47774
LENGTH: 25
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; ORGANISM: Probe Sequence
US-10-956-157-88877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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US-11-060-756-47774/c
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; ORGANISM: probe
US-11-060-756-47774
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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE REPRENCE: 031896-04300 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SEQ ID NO 42579
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: HUMAN OSTEOARTHITIS AND HUMAN PROTEASES FILE REFERENCE: 031896-043000 (Am 101081) CURRENT APPLICATION NUMBER: US/10/956,157 CURRENT FILING DATE: 2004-10-04 NUMBER OF SEQ ID NOS: 319805 SOFTWARE: PATENTIN VERSION 3.2
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                                                                               NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 980988
                                                                                                                                                                                                                                                   Length 25;
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10; Mismatches 5;
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CURRENT APPLICATION NUMBER: US/10/719,900 CURRENT FILING DATE: 2003-11-20 PRIOR APPLICATION NUMBER: 60/427,808 PRIOR FILING DATE: 2002 11 20
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"Sequence 42579, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
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Matches 11; Conservative
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                                                                                                                                                                                    ORGANISM: Mus musculus
US-10-719-900-980988
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US-10-956-157-88871
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                                                                                                                                                                             Sequence 276903, Application US/11136527

Fublication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William M
TITLE OF INVATION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT FILING DATE: 2005-05-25
FRICK RAPPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 276903
LENGTH: 25
                        Gaps
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 678730
LENGTH: 25
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                        Indels
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Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Nou
TITLE OF INVERTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT PILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
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  Best Local Similarity 47.4%; Pred. No. 5.5e+03;
Matches 9; Conservative 8; Mismatches 2;
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                                                               2 AUUGUCUCUCCUUUCGCCA 20
                                                                                          6 ATTGTCTGTCCTTTGGCCA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Probe US-11-136-527-276903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-678730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                         RESULT 10
US-11-136-527-276903
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
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; Sequence 276878, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; TILE REFERENCE: 011896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT APPLICATION NUMBER: US 60/574,294
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SEQ ID NO 276878
; LENGTH: 25
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Pred. No. 5.5e+03;
0; Mismatches 2; Indels
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45.8%; Pred. No. 4.5e+03;
tive 8; Mismatches 5; Indels
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FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 47788
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 205339, Application US/10310914A; Publication No. US20060003322A1; GENERAL INFORMATION:
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Best Local Similarity 89.5
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Best Local Similarity 45.8
Matches 11; Conservative
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                                                                                                                                                   ; TYPE: DNA
; ORGANISM: probe
US-11-060-756-47788
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LENGTH: 24
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; ORGANISM: Probe Sequence
US-10-956-157-21630
                                       Query Match
Best Local Similarity
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US-10-956-157-21624
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OF INVENTION: HUMAN OSTEDARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 498782
LENGTH: 20
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                              APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERBENCE: 365-41
CURRENT APPLICATION WUBER: US/11/036,317
CURRENT PILING DATE: 2005-01-13
PRIOR PAPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 35846
LENGTH: 25
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US-10-310-914A-498782
Sequence 498782, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Benwich, Isaac
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Best Local Similarity 40.9<sup>3</sup>
Matches 9; Conservative
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Best Local Similarity 94.1
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                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus musculus US-11-036-317-35846
                     APPLICANT: Williams,
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US-10-310-914A-498782
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LENGTH: 25
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Sequence 21630, Application US/10956157

| Publication No. US20050118625A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Wyell
| APPLICANT: Wyell
| TITLE OF INVENTION: HUAN OSTECARFREITIS AND HUMAN PROTEASES
| TITLE OF INVENTION: HUAN OSTECARFREITIS AND HUMAN PROTEASES
| TITLE OF INVENTION: HUAN OSTECARFREITIS AND HUMAN PROTEASES
| CURRENT APPLICATION HUMBER: US/10/956,157
| CURRENT PILING DATE: 2004-10-04
| NUMBER OF SEQ ID NOS: 319805
| SEQ ID NO 21630
| LENGTH: 25
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64.2%; Score 15.4; DB 10;
47.1%; Pred. No. 8.2e+03;
iive 8; Mismatches 1;
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                                                8; Conservative
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Matches 8; Conservative
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Query Match
Best Local Similarity 42.9
Matches 9; Conservative
RESULT 2
US-11-217-529-35946
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Sequence 35946, A
Sequence 171525,
Sequence 247873,
Sequence 247874,
Sequence 247876,
Sequence 247876,
Sequence 485166,
Sequence 485167,
Sequence 485168,
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Sequence 861056,
Sequence 8610°C,
Sequence 8610°C,
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Sequence 40426, A
Sequence 628721,
Sequence 848732,
                                                                             October 16, 2006, 14:16:55; Search time 53.2331 Seconds (without alignments) 842.395 Million cell updates/sec
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/ EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/ EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/ EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/ EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
/ EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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Sequence 4
Sequence 4
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          GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-217-529-35946

US-11-348-413-247873

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US-11-348-413-247874

US-11-348-413-247875

US-11-348-413-247875

US-11-348-413-485166

US-11-348-413-485167

US-11-348-413-485167

US-11-348-413-81058

US-11-348-413-81058

US-11-348-413-81058

US-11-348-413-81058

US-11-348-413-81058

US-11-348-413-81058

US-11-348-413-415777

US-11-348-413-40425

US-11-348-413-40425

US-11-348-413-40426

US-11-348-413-40425
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Match Length
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865459,
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIFKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT APPLICATION NUMBER: US 10/932,182
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR PRIOR OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
LENGTH: 25
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Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHHIRO
APPLICANT: NODAMA, YUKIKO
APPLICANT: FUJIMURA, TOWOKO
APPLICANT: FUJIMURA, TOWOKO
APPLICANT: ASHIKARI, TOSHHIKO
APPLICANT: ASHIKARI, TOSHHIKO
APPLICANT: ASHIKARI, TOSHHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
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                                                                    US-11-348-413-618728
US-11-348-413-978933
US-11-348-413-95262
US-11-348-413-251673
US-11-348-413-251673
US-11-348-413-251446
US-11-348-413-593446
US-11-348-413-65459
US-11-348-413-665459
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US-11-348-413-665459
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US-11-217-529-226417
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US-11-340-413-75095
US-11-348-413-80886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 uneucucuccunuceccaccu 23
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APPLICANT: Mysten
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mixphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: DCT/USO5/035471
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 247873
LENGTH: 25
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                                                                                                                                                                                    FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...[42]

OTHER INFORMATION: SEQ ID NO: 7205; WAN01UM2G; Start 113; Stop 137;

OTHER INFORMATION: 000000001100000

US-11-348-413-247872
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FRATURE:
NAME/KEY: misc feature
LOCATION: (1)...(25)
OTHER INFORMATION: SEQ ID NO: 7205; WANGIUM2G; Start 114; Stop 138;
COTHER INFORMATION: 000000001100000
US-11-348-413-247873
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59.2%; Score 14.2; DB 9;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3;
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 247872
LENGTH: 25
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; Sequence 247874, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
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                                                                                                         TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
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APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Oldsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/USOS/035471
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
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            FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PetentIn version 3.3
SOFTWARE: Patent 1 SE
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                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-35946
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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-171625
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Best Local Similarity 47.4
Matches 9; Conservative
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Matches 8; Conservative
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US-11-217-529-171625/c
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US-11-348-413-247872/C
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, Ellen
APPLICANT: Mounts, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: US/11/348,413
FRIOR APPLICATION NUMBER: US 11/243,445
PRIOR PILING DATE: 2005-10-05
PRIOR PILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 247876
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APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR PILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 485166
LIENGTH: 25
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                                                                                                                                                                                                                                Sequence 247876, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
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Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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OTHER INFORMATION: probe
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NAME/KEY: misc_feature
LOCATION: (1). (25)
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**APPLICANT: Mounts, William M
**APPLICANT: Murphy, Bilen
**TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT
**FILE REFREENCE: 03186-084100 (AM 10.724)

CURRENT APPLICATION NUMBER: US/11/348,413

CURRENT FILING DATE: 2006-02-07

PRIOR APPLICATION NUMBER: DCT/USO5/035471

PRIOR APPLICATION NUMBER: US 11/243,445

PRIOR FILING DATE: 2005-10-05

PRIOR FILING DATE: 2005-10-05

PRIOR FILING DATE: 2004-10-05

NUMBER OF SEQ ID NOS: 1276209

SEQ ID NO 247875

LENGTH: 25
                     APPLICANT: MULPHY, Bliam range of the control of th
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LOCATION: (1). (25)
OTHER INFORMATION: SEQ ID NO: 7205; WANOIUM2G; Start 115; Stop 139;
OTHER INFORMATION: 000000001100000
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; LOCATION: (1). (125)
; OTHER INFORMATION: SEQ ID NO: 7205; WANOIUM2G; Start 116; Stop 140;
; OTHER INFORMATION: 000000001100000
US-11-348-413-247875
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Pred. No. 3.1e+03;
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Mounts, William M
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Matches 9; Conservative
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Best Local Similarity 47.4
Matches 9; Conservative
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OTHER INFORMATION: probe
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ORGANISM: Artificial
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Olderdd, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REPERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: PCT/USOS/035471
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 485634
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; LOCATION: (1)...(25)
; OTHER INFORMATION: SEQ ID NO: 14505; WANGIUQIX; Start 1590; Stop 1614;
; OTHER INFORMATION: 00000000010000
US-11-348-413-485634
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PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 485168
TYPE: DNA
TYPE: DNA
ORGANISM: Artificial
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Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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OTHER INFORMATION: probe
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US-11-348-413-485635/c
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APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REPREMENCE: 03199-6084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/349,413
CURRENT FILING DATE: 2006-02-07
PRIOR FILING DATE: 2005-110-05
PRIOR FILING DATE: 2005-110-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
SEQ ID NOS: 1276209
SEQ ID NOS: 1276209
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APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Misted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 03.1896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
PRIOR APPLICATION NUMBER: PCT/USOS/035471
PRIOR FILING DATE: 2005-10-05
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                                                     LOCATION: (1) ... (25)
COTHER INFORMATION: SEQ ID NO: 14491; WANGIUGID; Start 1353; Stop 1377;
COTHER INFORMATION: 00000000001000
US-11-348-413-485167
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Pred. No. 3.1e+03;
7; Mismatches 3; Indels
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S9.2%; Score 14.2; DB 9;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3;
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Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Woute, William M
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Best Local Similarity 47.4%;
Matches 9; Conservative
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                             NAME/KEY: misc_feature
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ORGANISM: Artificial
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US-11-348-413-485168/c
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Onnered, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: US/11/348,413
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR PLLING DATE: 2005-10-05
PRIOR PLLING DATE: 2004-10-05
PRIOR PLLING DATE: 2004-10-05
PRIOR FILING DATE: 2004-10-05
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LOCATION: (1). (25)
OTHER INFORMATION: SEQ ID NO: 7205; WANOIUM2G_at; Start 114; Stop 138;
OTHER INFORMATION: 00000001100000
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Best Local Similarity 47.4%; Pred. No. 3.18+03;
Matches 9; Conservative 7; Mismatches 3;
                                                                                                                                                                                                            9; Mismatches
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Ubblication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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US-11-348-413-861056/c
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Olmsted, Stephen
ITTLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-064100 (AM 101734)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-10-06
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR PILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
PRIOR FILING DATE: 2004-10-05
SEQ ID NO 485635
LENGTH: 25
TYPE: ...
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## APPLICANT: Mounts, William M
## APPLICANT: Mounts, Ellen
## APPLICANT: Murphy, Ellen
## APPLICANT: Olmsted, Stephen
## TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFPERENT SPECIES
## CURRENT FILING DATE: 2006-02-07
## CURRENT FILING DATE: 2005-10-05
## PRIOR APPLICATION NUMBER: PCT/US05/035471
## PRIOR PILING DATE: 2005-10-05
## PRIOR PAPLICATION NUMBER: US 11/243,445
## PRIOR PILING DATE: 2005-10-05
## PRIOR PILING DATE: 2004-10-05
## PRIOR FILING DATE: 2005-10-05
## PRIOR FILING DATE: 2005-10-0
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; LOCATION: (1). (25)
; OTHER INFORMATION: SEQ ID NO: 2332; WANOIUMKM_at; Start 686; Stop 710;
; OTHER INFORMATION: 1111111100000000
US-11-348-413-689385
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Pred. No. 3.1e+03;
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Pred. No. 3.1e+03;
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US-11-348-413-689385/c
; Sequence 689385, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
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Best Local Similarity 47.4%;
Matches 9; Conservative
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AX215299 Sequence
AX215300 Sequence
AR00081 Sequence
AR179914 Sequence
132528 Sequence 48
143473 Sequence 48
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AR44659 Sequence
AR44659 Sequence
AR44659 Sequence
AR49659 Sequence
A7936 Sequence 12
A7936 Sequence 12
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A7936 Sequence
AR03177 Sequence
BD007603 NematodaAR301217 Sequence
AR032175 Sequence
AR0323175 Sequence
AR0323175 Sequence
AR06263 Sequence

Sequence:

Run on:

Searched:

Database

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BD232707 30 bp DNA linear PAT 17-JUL-2003 Therapeutic and diagnostic domain 1-beta-2GPI polypeptide and method of using the same.

BD232707 GI:33042477
                                                                                                                                                                                                                                                                                                                                                                                          Majumder, K., Spytek, K.A., Tchernev, V.T., Colman, S.D., Padigaru, M., Zerhusen, B., Gusev, V., Burgess, C., Li, L., Malyankar, U.M., Gangolli, E., Scone, D., Macdougall, J., Smithson, G. and Ellerman, K. Novel proteins and nucleic acids encoding same Patent: WO 0194416-A 70 13-DEC-2001; Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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// Organism="synthetic construct"
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synthetic construct
other sequences, artificial sequences.
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Sequence 70 from Patent WO0194416.
AX399122
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         AX215300
AR080081
AR179914
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132528
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AR181963
AR494659
AR24876
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AR032177
BD007603
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AR372695
AR015990
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AK413910 Sequence
AX4413910 Sequence
AX447885 Sequence
AX24378 Sequence
AX24378 Sequence
AX064751 Sequence
AR06237 Sequence
AR137020 Sequence
BD105661 Genes sen
177021 Sequence 81
181112 Sequence 81
181112 Sequence 81
CS226910 Sequence
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CS226910 Sequence
CS226910 Sequence
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BD232707 Therapeut
                                                             ; Search time 2092.41 Seconds (without alignments) 2597.742 Million cell updates/sec
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                                                                                                                   ggguuaucugcaacugagag.....uuuucuggaugcagaguccu
         . GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                 1796954
                                                                                                                                                              6366136 segs, 31973710525 residues
                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                            nucleic search, using sw model
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AX443910
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AX73082
AX73082
AR770823
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PAT 27-MAY-2002

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Result Š. 26;

PAT 03-JUL-2002

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/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="Computer Generated Probe Sequence."
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Corganism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe
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18.6*; Score 15.8; DB 2;
Best Local Similarity 73.7*; Pred. No. 1.8e+06;
Matches 14; Conservative 3; Mismatches 2;
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Patent: WO 0216649-A 4341 28-FEB-2002;
Illumina, Inc. (US)
Location/Qualifiers
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Patent: WO 0215649-A 365 28-FEB-2002;
Illumins, Inc. (US)
Location/Qualifiers
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AR770823
LOCUS AR770823 28 From patent US 6965010.
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  23
                        25 UGGUUAAGGCGUCCCCAAGUUGGAAGGGC
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AX447886
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                                                                                                                                                 Linnik M.D.

Therapeutic and diagnostic domain 1-beta-2GPI polypeptide and method of using the same

Patent: JP 2002517245-A 8 18-JUN-2002;

LA JOLLA PHARMACEUTICAL CO
OS Artificial Sequence
PN JP 2002517245-A/8
PD 18-JUN-2002
PP 09-JUN-1999 JP 2000553585
PR 09-JUN-1999 US 60/088656,05-OCT-1998 US 60/103088 PR 09-JUN-1999 US 09/328199
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                     synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 30)
Marquis,D.M., Iverson,G.M., Victoria,E.J., Jones,D.S. and Linnik,M.D.
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1 (bases 1 to 30)
Marquis, D.M., Iverson, G.M., Victoria, E.J., Jones, D.S. and
Linnik, M.D.
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Location/Qualifiers
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19.1%; Score 16.2; DB 2; Length 30;
Best Local Similarity 58.6%; Pred. No. 1.3e+06;
Matches 17; Conservative 4; Mismatches 8; Indels
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    .30
    ^organism="synthetic construct"
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Sequence 18 from patent US 6858210.
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Unknow...
Unclassified.
1 (bases 1 to 30)
Skolnick, M.H., Goldgar, D.E., Miki, Y., Swenson, J., Kamb, A.,
Harshnan, K.L., Shattuck-Eidens, D.M., Tavtigian, S.V., Wiseman, R.W.
and Futreal, P.Antrew.
17q-linked breast and ovarian cancer susceptibility gene
Patent: US 6162897-A 81 19-DEC-2000;
Location/Qualifiers
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Schlatch, M. H., Goldgar, D.E., Miki, Y., Swenson, J., Kamb, A.,
Harshman, K. D., Shattuck-Eidens, D.M., Tavtigian, S.V., Wiseman, R.W.
and Futreal, P.Andrew.
170-linked breast and ovarian cancer susceptibility gene
Patent: NG 5753441-A 81 19-MAY-1998;
Location/Qualifiers
Harshman, K.D., Shattuck-Eidens, D.M., Tavtigian, S.V., Wiseman, R.W. and Futreal, P.Andrew.
17Q-linked breast and ovarian cancer susceptibility gene Patent: US 5747282-A 81 05-MAY-1998;
Location/Qualifiers
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Best Local Similarity 36.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 10; Mismatches 6;
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/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"
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/wol_type="unassigned DNA"
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AR008237.1 GI:3967346
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                                                                                                        1 (bases 1 to 28)
Altalo, K. and Jelsch, M.W.
Materials and methods involving hybrid vascular endothelial growth factor DNAs and proteins
Patent: US 6965010-A 28 15-NOV-2005;
Licentia, Ltd. and Ludwig Institute for Cancer Research; Helsinki; FIX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alitalo, K.M. and Jeltsch, M.M.
Materials and methods involving hybrid vascular endothelial growth
factor dasa and proteins and screening methods for modulators
Factor than and proteins and screening methods for modulators
Patent: WO 0162942-A 28 30-AUG-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US); Licentia OY (FI)
Location/Qualifiers
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Unclassified.
1 (bases 1 to 30)
Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
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/mol type="unassigned DNA"
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/db xref="taxon:32630"
/noTe="oligonucleotide"
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Sequence 81 from patent US 5747282.
AR004751
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AX234378
AX234378.1 GI:15593379

    .28
    /organism="unknown"
    /mol_type="genomic DNA"

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AR770823.1 GI:83346139
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Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Harshman,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W.
and Futraal,P.Andrew.
17q-linked breast and ovarian cancer susceptibility gene
Patent: US 5710001-A 81 20-JAN-1998;
Location/Qualifiers
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Shattuck-Bidens, D.M., Simard, J., Durocher, F., Emi, M. and
Nakamura, Y.

    (bases 1 to 30)
    Shattuck-Eidens, D.M., Simard, J., Durocher, F., Emi, M. and

                                                                                                                                                Linked breast and ovarian cancer susceptibility gene Patent: US 5693473-A 81 02-DEC-1997; Location/Qualifiers
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Best Local Similarity 36.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 10; Mismatches 6;
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 30)
Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Harshman,K.D., Eidens,D.M.S., Tavtiglan,S.V., Wiseman,R.W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1994 US 08/289221,02-SEP-1994 US 08/300266 PR 16-SEP-1994 US 08/348824 PR 24-MAR-1995 US 08/340305,07-JUN-1995 US 08/483554 PR 07-JUN-1995 US 08/487002 PI MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE WARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E GOLDGAR, YOSHIO MIKI, JEFF SWENSON, PI DE MARK H SKOLNICK, DAVID E MARK H SKOLNICK, DAV
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Strandedness: Single;
Topology: Linear;
Genes sensitive to 17q-chained breast cancer and ovarian
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Sequence 81 from patent US 5693473.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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12-AUG-1994 US 08/289221
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Homo sapiens (human)
Homo sapiens
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Methods, compositions and compound assays for inhibiting amyloid-beta protein production Patent: WO 2005103713-A 12 03-NOV-2005; Galapagos Genomics N.V. (BB)
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                                Query Match
Best Local Similarity 36.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 10; Mismatches 6; Indels
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                                                                                                                                                                                                                       CS226910 21 bp DNA Sequence 12 from Patent WO2005103713. CS226910.1 GI:83691771
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                        6 CTCTGCTTGTGTTCTCTGTCTCCAG 30
                                                                                                    55 CUTUGCUUCUGUUUUCUGGAUGCAG 79
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Homo sapiens
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Search completed: October 16, 2006, 14:52:14 Job time : 2094.41 secs

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Sequence 15707, A
Sequence 18, Appl
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10621, A
20972, A
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GenCore version 5.1.9
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US-09-328-199-18
US-09-396-196G-12452
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0.000000000000000000000000000000000000		RESULT 1  US-09-396-196G-15707/c  Sequence 15707, Application US/093961966  Batent No. 6821724  GENERAL INFORMATION:  APPLICANT: Michael Mittmann  APPLICANT: David Mack.  CURRENT APPLICATION NUMBER: US/09/396.  CURRENT APPLICATION NUMBER: 60/100,678  PRIOR FILING DATE: 1998-09-15  PRIOR FILING DATE: 1998-09-17  NUMBER OF SEQ ID NOS: 127806  SOFTWARE: FastSEQ for Windows Version SEQ ID NO 15707  LENGTH: 25  TYPE: DAM  ONGANISM: Mus musculus  US-09-396-196G-15707  Query Match  Best Local Similarity 60.0%; Score I'  Best Local Similarity 60.0%; Pred. NM matches 15; Conservative 5; Mismatches 15; Conservative 5; Mismatches 15; Conservative 5; Mismatches 15; Conservative 5; Mismatches 15; Conservative 60.0%; Sequence 18, Application US/09328199
44444444444444444444444444444444444444	*	RESULT 1  US-09-396-196G-15707/c Sequence 15707, Appl Patent No. 6821724 APPLICANT: Michael APPLICANT: David M. TITLE OF INVENTION: FILE REFERENCE: 310 CURRENT FILING DATE: NUMBER OF SEQ ID NO. CURRENT APPLICATION NO. CURRENT APPLICATION NO. FILE REFERENCE: 30 CURRENT APPLICATION NO. CURRENT APPLICATION NO. CURRENT APPLICATION NO. SOFTWARE: FESTSOF F. LENGTH: 25 TYPE: DNA ORGANISM: MUS MUS MUSCOFF BEST LOCAL SIMILATIC MATCHS 15; CONSE MATCHS 15; CONSE MATCHS 15; CONSE ONE APPLICANT: WARDICANT: APPLICANT: WARDICANT: APPLICANT: WARDING: APPLICANT: MATCHS SEGIO GENERAL INFORMATION: APPLICANT: LIMIK, TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: 252.
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18.8%; Score 16; DB 3; Length 25;
Best Local Similarity 45.8%; Pred. No. 1.1e+04;
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US-09-396-196G-119518
Sequence 119518, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FRSESE (or Windows Version 4.0)
SEQ ID NO 119518
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Patent No. 6821724
GENERAL INPORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
TILE REPERENCE: 3101.1
CURRENT APPLICATION WHERE: US/09/396,196G
CURRENT APPLICATION WHORE: 60/100,678
PRIOR PILLING DATE: 1998-09-15
PRIOR FILLING DATE: 1998-09-17
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Matches 11; Conservative
; SEQ ID NO 119516
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-119516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CRGANISM: mus musculus
US-09-396-196G-119517
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Pred. No. 9.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
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US-09-196-119516

Sequence 119516, Application US/09196196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: 190-01.1

CURRENT PILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER: PSECTION NUMBER: 1998-09-17

NUMBER: OF SECTION NUMBER: 1998-09-17

NUMBER: OF SECTION NOW VETSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.1%; Score 16.2; Dest Local Similarity 58.6%; Pred. No. 9.7e Matches 17; Conservative 4; Mismatches
CURRENT FILING DATE: 1999-06-09
EARLIER APPLICATION NUMBER: 60/088,656
EARLIER FILING DATE: 1990-06-09
EARLIER FILING DATE: 1990-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TGGTGATGGTGGCCACAACTTGGCATGGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 UGGUUAAGGCGUCCCCAAGUUGGAAGGGC 53
                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: synthetic construct US-09-328-199-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 UUCUGUUUUCUGGAUGCAGAGUCC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 TIGICITCICIGGATCAAGAGICC 1
                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.78;
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Best Local Similarity 41.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Mus musculus
US-09-396-196G-2452
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Gaps
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Fatent No. 6965010
GENERAL INFORMATION:
APPLICANT Alitalo et al
TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
FILE REFERENCE: 28967/359778
CURRENT APPLICATION NUMBER: US/09/795,006A
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/205,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       18.1%; Score 15.4; DB 3; Length 25; 60.0%; Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50927, Application US/09396196G
; Sequence 50927, Application US/09396196G
; Patent No. 68212AD;
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Methods of Genetic Analysis
; TILE OF INVENTION: Methods of Genetic Analysis
; FILE REPRENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1998-09-15
; PRIOR PILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50927
                                                               APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1.1
CURRENT APPLICATION WUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION WUMBER: 60/100,678
PRIOR APPLICATION WUMBER: 60/100,678
PRIOR ELLING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 CAAGUUGGAAGGGCGCUUUGCUUCU 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAAGCTGGAAGGCCGCGAGGCTTAT 25
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25 CTTGTGTCATCTGTGAAGAGTCC 1
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 60.0 Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Mus musculus
US-09-396-196G-20972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-396-196G-50927/c
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Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                Sequence 10620, Application US/09396196G; Patent No. 6821724; Patent No. 6821724; GENERAL INFORMATION: APPLICANT: Michael Mittmann; APPLICANT: David Mack, APPLICANT: David Lockhart, APPLICANT: David Lockhart, TITLE OF INVENTION: Methods of Genetic Analysis; FILE REFERENCE: 310.1.1 CURRENT APPLICATION NUMBER: US/09/396,196G; CURRENT FILING DATE: 1999-09-15; PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17; NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FREESEQ for Windows Version 4.0; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
FRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PSESSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 10621
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.1%; Score 15.4; DB 3; 68.0%; Pred. No. 1.8e+04; tive 2; Mismatches 6;
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68.0%; Pred. No. 1...
'... 2; Mismatches
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Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
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                                               1 CIGITIGCIGCIACAAAGICC 22
                           63 CUGUUUUCUGGAUGCAGAGUCC
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Best Local Similarity 68.01
Best Local 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 68.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-10620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-10621
                                                                                                                                    RESULT 7
US-09-396-196G-10620
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US-09-396-196G-20972
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US-09-396-196G-10621
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APPLICANT:
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APPLICANT: SACINICK, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Wiki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Swenson, Jeff
APPLICANT: Harshman, Keith D.
APPLICANT: Tavrigian, Sean V.
APPLICANT: Tavrigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Succeptibility Gene
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable.
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.1%; Score 15.4; DB 2; Length 30; Best Local Similarity 36.0%; Pred. No. 2e+04; Matches 9; Conservative 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Jene
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
CONTRY: USA
ZIP: 200A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALP: 20005
CAPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,553
FILING DATE: 24-MAR.1995
RICH DATE: 24-MAR.1995
FILING DATE: 24-MAR.1995
FILING DATE: 24-MAR.1995
FILING DATE: 24-MAR.1995
FILING DATE: 16-SEP-1994
FILING DATE: 16-SEP-1994
PRICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRICATION NUMBER: US 08/300,266
PRICATION NUMBER: US 08/300,266
                                                                               24884-109347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 CUUUGCUUCUGUUUUCUGGAUGCAG 79
ATTORNEY/AGENI INC......

NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2488.
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFRX: 202-962-8300
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-480-784-81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                              FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: Artificial chimeric
OTHER INFORMATION: Oligonucleotide sequence derived from multiple vertebrate vascula
CTHER INFORMATION: endothelial growth factor
US-09-795-006A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Goldgar, Yoshio
APPLICANT: Wish, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Harshman, Keith D.
APPLICANT: Harshman, Keith D.
APPLICANT: Harshman, Keith D.
APPLICANT: Haseman, Roger W.
APPLICANT: Pavigian, Sean V.
APPLICANT: Pavigian, Sean V.
APPLICANT: Putrail, P. Andrew:
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                Query Match
18.1%; Score 15.4; DB 4; Length 28;
Best Local Similarity 64.0%; Pred. No. 1.9e+04;
Matches 16; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: J201 New York Avenue, N.W., Suite 1000 CITY: Washington STATE: DC COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER: PLOSPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-MOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 12-AUG-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 12-AUG-1994
PRIOR FILING DATE: 2000-05-18
PRIOR PEDLICALION NUMBER: US 60/185,205
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 175
SSOFTWARE: Patentin Ver. 2.0
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGUUAUCUGCAACUGAGAGGGGCUG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GGGTTGCTGCAATAGTGAGGGGCTG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 81, Application US/08480784 Patent No. 5693473
                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20002
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US-08-480-784-81
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APPLICANT: Swenson, Jeff
APPLICANT: Swenson, Jeff
APPLICANT: Swenson, Jeff
APPLICANT: Harshwan, Keith D.
APPLICANT: Harshwan, Keith D.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Putreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Beatjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.1%; Score 15.4; DB 2; Length 30; 36.0%; Pred. No. 2e+04; tive 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISP Compatible
SOSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,554B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-MOV-1994
PRILING DATE: 29-MOV-1994
PRILING DATE: 29-MOV-1994
PRILING DATE: US 08/308,104
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGASTRANTON NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2484-109347
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION SEQ 1D NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS CUTUGCUUCUGUUUUCUGGAUGCAG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 CTCTGCTTGTTTCTCTGTCTCCAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-483-554B-81
; Sequence 81, Application US/08483554B
; Patent No. 5747282
                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skolnick, Mark H.
Goldgar, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 36.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Simard, Jacques
APPLICANT: Emi, Mitsuru
APPLICANT: Emi, Mitsuru
APPLICANT: Durocher, Francine
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:.
APPLICATION NUMBER: US/08/487,002
  FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REFERENCE/DOCKET NUMBER: 24.894-109347
TELECOMMUNICATION INFORMATION:
TELEFAN: 202-962-4810
TELEFAN: 202-962-4810
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305

FILING DATE: 24-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824

FILING DATE: 29-MOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104

FILING DATE: 16-SEP-1994

PRIOR APPLICATION NUMBER: US 08/300,266

FILING DATE: 02-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 CTCTGCTTGTGTTCTCTGTCTCCCAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 CUUUGCUUCUGUUUUCUGGAUGCAG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 81, Application US/08487002
Patent No. 5710001
                                                                                                                                                                                                                                                                                                                          LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Homo sapiens US-08-483-553-81
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: DC
COUNTRY: US
ZIP: 20005
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US-08-487-002-81
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Gaps

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PILING DATE: 16-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/300,266
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
PRIOR APPLICATION NUMBER: US 08/289,221
PRIOR APPLICATION NUMBER: US 08/289,221
PRIOR APPLICATION NUMBER: US 08/289,01
PREMEMCE/DOCKET NUMBER: 2484-109347
PRICEPRIOR 202-962-8300
PREMEMCE/DOCKET NUMBER: 26-262-8300
PREMEMCE/DOCKET NUMBER: 28-262-8300
PREMEMCE/US TYPE: NUMCIE CHARACTERISTICS:
LENGTH: 30 base pairs
PREMEMCE/US TYPE: DAA (genomic)
PROPOLOGY: linear
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Search completed: October 16, 2006, 14:47:13 Job time : 197.842 secs

8 &

AJ57468 Arabidops AJ57468 Arabidops AJ527468 Arabidops AZ320101 1M0040804 AZ320101 1M0040804 AZ320379 Pan trogl CZ469769 C0113-3p CZ469769 C0113-3p AZ375590 1M01291A12 AZ375590 1M01291A12 AZ375590 1M012541 BH790976 SALK D583 CZ481452 e03694-5p AZ30550 1M0016A11 CZ194878 PST13293-CZ488898 F06234-5p AZ479371 T. brucei BZ356062 SALK 1280 AZ479632 T. brucei CZ11022 ABF-06-B CX011229 io51b09.b DV227849 EST-AR161 AZ802448 ZM0061B20 AJ598500 Arabidops

Run on:

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4018012H11.1EL y1 4018 - RescueMu Grid X Zea mays genomic, genomic c2910028.1 G1:71923396 GSS.08-AUG-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
(pases 1 to 25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Biological Sciences
Stanford University
Stanford University
Stanford University
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4018012 row: H column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                A1143800
AZ320101
AZ320101
CZ469769
CZ471273
AZ375590
AZ876196
AZ876196
AZ832180
BH790976
CZ194878
CZ194878
CZ194878
CZ194878
CZ194878
CZ194878
CZ194878
CZ194878
CZ19409P
BH851575
AZ788334
ATH527468
                                                                                                                                                                                                                                                                                                                                                                                  DV227849
AZ802448
AJ598500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays
Zea mays
 Walbot, V.
 RESULT 1
CZ910028/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
   CZ910028 4018012H1
HZ5855 y153h65.s1
AZ814281 ZM0082L04
AZ81302 1M0376A16
B192920 W02830987
B2292979 SALK 1290
AZ469472 1M0283A06
AZ785027 ZM028H03
AZ865300 ZM0028H03
AZ865300 ZM068F13
BF732161 EST-NGR-1
AZ763057 1M0558C22
AJ591134 Arabidops
BH999983 SALK 0648
BH809983 SALK 0648
BH99983 SALK O648
                                                                                                              ; Search time 3655.64 Seconds (without alignments) 1300.222 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                   1 ggguuaucugcaacugagag.........
                  GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                   56556
                                                                                                                                                                                                                                                                                                 48236798 segs, 27959665780 residues
                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ469472
AZ806300
BF732161
AZ50300
BF732161
AJ591134
BH792654
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BH792654
BH792654
BH792654
BH792654
BH792654
AA961904
CZ482297
CZ482297
CZ482297
                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                nucleic search, using sw model
                                                                                                                 October 16, 2006, 14:04:23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ814281
AZ583022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CZ910028
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Gapop 10.0 , Gapext 1.0
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85
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90 est3::

90 est5::

90 est6::

90 est6::

90 est7::

90 est7::

90 est7::

90 est8::

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Match Length
                                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST: *
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116.19
116.19
116.19
116.19
115.18
115.18
115.18
115.18
115.18
115.18
                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                               Scoring table:
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4.1
4.1.4
1.4.1
1.2
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Maximum DB
                                                                                OM nucleic
                                                                                                                                                                                                                   Sequence:
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Database

CZ482297 e04545-5p AJ531105 Arabidops CZ471342 d00034-5p

Result g OU

8

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Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.murransposon.org/project/RescueMu/', Grid X was grown at UCSD in 2003. DNA was extracted from leaf strips, double digested using Bamali and Balli, and ligated to form circular plasmids. DHIOB cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H25855

yl53h05.81 Soares breast 3NbHBst Homo sapiens cDNA clone
IMAGE:162009 3' similar to gb:S71043_rna1 IG ALPHA-2 CHAIN C REGION
(HUMAN); mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
Insert Size: 934
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 934 Std Error: 0.00
Seq primer: Promega -21m13
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.

1 (bases 1 to 30)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project Unpublished (1995)
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                19.1%; Score 16.2; DB 13; Length 25; 38.1%; Pred. No. 1.3e+06;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                            3,
                                                                                                                                                                                                                                                               10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
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/db xref="taxon:9606"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                      23 GGCTCTTTGTTTTGTTTTC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H25855.1 GI:894978
                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                    Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                   Query Match
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SOURCE
ORGANISM
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
H25855/c
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreasis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|ABL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 22)
Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS 20-FEB-2001
and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot 20. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ814281
2M0082L04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0082L04 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroldea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                           ö
                                                                                                                                                                       Length 30
                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                     Score 16; DB 10;
Pred. No. 1.5e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunngenetics.utah.edu
10art Length: 10000 Std Error: 0.00
Plate: 0082 row: L column: 04
                                                                                                                                                                     Query Match
18.8%; Score 16; DB
Best Local Similarity 66.7%; Pred. No. 1.5e
Matches 16; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: 0082 row: L column: 04
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/clone="UUGC2M0082L04"
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Location/Qualifiers
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AZ814281.1 GI:12984285
GSS.
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KEYWORDS
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D19580/c
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored to competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ583022 28 bp DNA linear GSS 13-DEC-2000
1M0376A16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murcidea; Muridae; Murinae; Mus.

1 (bases 1 to 28)
1 (bases 2 to 28)
1 (bases 2 to 28)
1 (bases 3 to 28)
1 (bases 2 to 28)
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Contact: Robert B. Weiss
Contversity of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="E. Coli strain XLIO-Gold, Ti-resistant, F-" /clone_lib="Mouse_l0kb plasmid_UUGCIM_library" /note=""Vector: PUTFIFIE OF PARTY PA
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                   Score 15.4; DB 11; Length 22; Pred. No. 2.3e+06;
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Fax: 801 585 7177
Email: ddunnogenetice.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0376 row: A column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
                                                                                                                                                                                                                                                                                                                                                                                                                     8; Mismatches
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0376A16"
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AZ583022.1 GI:11702488
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                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-GGld (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 3'-directed"
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sclurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.
Analysis of gene expression in mouse embryogenesis by 3'-directed
cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D19580 25 bp mRNA linear EST 09-FEB-;
MUSGS00987 Mouse 3'-directed Mus musculus cDNA clone mb1686 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1995)
Contact: Shoko Kawamoto
Institute for Cellular and Molecular Biology
                                                                                                                                                                                                                          ch 18.1%; Score 15.4; DB 11;
1 Similarity 44.0%; Pred. No. 2.4e+06;
11; Conservative 8; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: shoko@next.imcb.osaka-u.ac.jp.
Location/Qualifiers
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/clone="mb1686"
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                                                                                                                                                                                                                                                                                                                                             56 UUUGCUUCUGUUUUCUGGAUGCAGA 80
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/strain="C57BL/6J"
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BZ292979
BZ292979.1 GI:24340856
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Plate: 0283 row: A column: 06
Seg primer: CGTYCTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
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                                                                                                                                                                                                                                                                     sex="Male"
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Fax: 801 585 7177
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Best Local Similarity
Matches 6; Conserva
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/clone="SALK 129051.26.25.x"
/clone="SALK 129051.26.25.x"
/clone lib="Azabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Azabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 29)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
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                                                                                                                                             Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Kose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weises, R., Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
/mol_type="genomic_DNA"
/ecotype="Col-0"
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Fax: 801 585 7177
Taball: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymcleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gil 4732114[gb]AR12972.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0028H03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0028H03 R, genomic survey sequence.
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Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, K., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                          /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note=""ector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/organism="Mus musculus
                                    /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                 db_xref="taxon:10090"
                                                                                                                                                     clone="UUGC1M0283A06"
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Inducatory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared bNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xi10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Chen,J., Rowley,D.A., Clark,T., Lee,S., Zhou,G., Beer,C.,
Rowley,J.D. and Wang,S.M.
Pattern of gene expression in mouse GR-1+ myeloid progenitor cells
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UGCIM library" | hote="Vector: PWD42nv; Purified genomic DNA from M. musculus G578L/6J (male) was obtained from the Jackson
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5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
Tel: 772-702-6788
Fax: 773-702-3002
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   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0068 row: F column: 13
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                 /db xref="taxon:10090"
/clone="UUGC2M0068F13"
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Hem/Onc
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Fer: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ806300 24 bp DNA linear GSS 20-FEB-2001 2M0068F13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0068F13 F, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XLIO-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weise, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Pred. No. 5.9e+06;
4; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
         Std Error: 0.00
Insert Length: 10000 Std Brror: C Plate: 0028 row: H column: 03 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends ends top: 23. High quality sequence stop: 23.
                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                     xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                 /clone="UUGC2M0028H03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 63.2%;
                                                                                                                                                                                                                                                                                                                                                                   /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
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AJ591134/c
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DEFINITION
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fragments from SAGE tags for Gene Identification, Proc. Natl. Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till the last CATG site of the target cDNA sequence. Seq primer: M13 Forward.
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1M0558C22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UGGIM library"
/note="Vector: PWD42Ivv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                    /tissue type="bone marrow"
/cell_type="GR-1+ myeloid progenitor cells"
/clone_lib="mouse GR-1+ myeloid progenitor cells cDNA
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                             15.8%; Score 13.4; DB 2; Length 26; ilarity 26.1%; Pred. No. 1.1e+07; Conservative 11; Mismatches 6; Indels
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Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
linsert Length: 10000 Std Error: 0.00
Plate: 0558 row: C column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
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/mol_type="genomic DNA"
                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
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                                                                                                                                                         /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
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/clone="UUGC1M0558C22"
                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                     /sex="female"
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                                                                                                                                                                                                                                                                                                   Library
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
tes 6; Conserv
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwhoz (gil 47321141gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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FOR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequence from the left or the right border to determine the genomic sequence flanking the insertion T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at thtp://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AJ591134 27 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)
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SSS. 1eft border, T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Busaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/ecotype="Wassilewskija"
1. .27
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/mol_type="qenomic DNA"
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Balzergue, S.
Direct Submission
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LOCUS

RESULT 13 BH792654/c

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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DN955347 27 bp mRNA linear EST 04-MAY-2005
it86c09.gl Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
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Bukaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Varidiplantae; Gnetopsida; Gnetales; Gnetaceae; Gnetum.
1 (bases 1 to 27)
Brenner, E.D. Trigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
Brandpnesy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
                                                                                                                                                                           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases I to 29) Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Shinn, P., Zimmerman, J., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R. A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome (2001)
                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="taxon:3702"
/clone="SALK 036896"
/clone="SALK 036896"
/clone="Fazabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used car
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is single pass sequence recovered from the left border of
thaliana genomic clone SALK_036896, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%; Score 13.4; DB 11; Length 29; ilarity 43.5%; Pred. No. 1.1e+07; Conservative 7; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                  Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
101010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Arabidopsis thaliana"
                                                                                                   Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: TDNA tagged.
Location/Qualifiers
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                        BH809983 -
BH809983.1 GI:20387800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ecker@salk.edu
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AUTHORS
                                                                                                                                                                                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                     BH792654 10.x Arabidopsis thaliana TDNA innear GSS 02-APR-2002 SALK 064849.48.70.x Arabidopsis thaliana genomic clone SALK_064849.48.70.x, genomic
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/clone="SALK 06449.48.70.x"
/clone="lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaeae; Arabidopsis.

(bases 1 to 29)
Alonso,Ju, Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is single pass sequence recovered from the left border of
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                                                                                                      Length 27;
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                                                                                                   Score 13.4; DB 14;
Pred. No. 1.1e+07;
3; Mismatches 1;
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  /note="T-DNA flanking sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic_DNA"
/ecotype="Col-0"
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Location/Qualifiers
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23 TIGGAGCGGIGCTAIGAIGCIGI 1
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                                                                                                15.8%;
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                                                                                        Query Match
Best Local Similarity 73.3 Matches 11, Conservative
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source

FEATURES

LOCUS DEFINITION

RESULT 14 BH809983/c

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ORIGIN

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Gaps

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Tel: 516 367 8884

Fax: 516 367 8874

Email: mccombie@cshl.org

Seq primer: -2IM13UnivRev.

Location/Qualifiers

i..27

/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/slone lib="Gretum female cone (NYBG)"
/note="Organ: matuer, unfertilized reproductive strobil;
/clone lib="Gretum female cone (NYBG)"
/note="Organ: matuer, unfertilized reproductive strobil;
/vector: pBK-CKV; Site=1: Xhoi; Site=2: Eco Ri; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZaP Express CDNA Synthesis Kit. The
library was alize-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"
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15.5%; Score 13.2; DB 9; Length 27;
Best Local Similarity 50.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 6; Mismatches 3; Indels
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Search completed: October 16, 2006, 15:51:26 Job time : 3658.64 secs

Aci82438 Human mic Aas12826 Human VEG

Adx84134 DNA ampli Adx75812 Chimeric Ad61714 Anti-NRID Aee01688 G protein Aee01687 G protein Acx6430 Human mic Aec7632 Human Hun Adx99810 PCR prime Abx60741 Human NOG Abx60742 Human NOG Abx60742 Human NOG Abx60742 Human NOG Abx60742 Human NOG Abx60749 Human NOG Acs9288 Human IRT Acx78730 Dengue vi Acx8730 Dengue vi Acx8730 Dengue vi Acx8730 Human RT Acx8730 Human RT Acx8730 Human RT Acx8730 Human RT Acx8730 Human mic Acx8655 Human mic Acx8650 Human mic Acx8650 Human mic Acx8650 Human mic Acx865178 Human mic Acx8655 Human mic

AEF08297
AC182438
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ADC61714
AEE01687
AEE01687
AEE07632
ACX26430
AAT74315
AEE07632
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October 16, 2006, 13:53:09 ; Search time 444.812 Seconds (without alignments) 1332.341 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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11: geneseqn1980s:*
2: geneseqn1990s:*
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4: geneseqn201as:*
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7: geneseqn201as:*
 GenCore (c) 1993
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                                                   OM nucleic
                                                                                                                                                             Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aad25159 Human NOV	Adk51090 Human NOV	Ade03643 BGS PCR p	Aah74161 Human neu	Aaz29694 Oligonucl	Aed56453 Human ost	Abq11002 Oligonucl	Abq04674 Oligonucl	Abq04715 Oligonucl	Abq00358 Oligonucl	Abq11043 Oligonucl	Abq12538 Oligonucl	Abq12579 Oligonucl		-	Adx84276 DNA ampli	Aed57194 Human ost	Aed57246 Human ost
SUMMARIES	ID	AAD25159	L ADK51090	) ADE03643	AAH74161	AAZ29694	AED56453	ABQ11002	ABQ04674	ABQ04715	ABQ00358	ABQ11043	ABQ12538	ABQ12579	4 ADY01452	1 ADY03184	1 ADX84276	1 AED57194	1 AED57246
	% Query Match Length DB	26 6	26 11	23 1(	29 4	30 3	30 14	24 6	24 6	24 6	24 6	24 6	25 6	25 6	30 14	30 14	30 14	30 14	30 14
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standard; DNA; 26 BP.	(first entry)	Human NOV4 gene expression assessing Ag1252 probe.	Human; NOV4; gene therapy; atherosclerosis; cardiomyopathy; leukaemia;	neurological; neurodegenerative disease; cell signalling; inflammation; disberge: seizure: muscular dystronby: enilensy: allergy: adenocarcinom	coagulation disorder; reproductive; respiratory; bone; nephrological;	multiple sclerosis, mental depression, gastro-intestinal disease, cancer,	utinaty system atsoluci; nautson s atsoase; migratus; dermacomyositis; bronchitis; probe; ss.		Location/Qualifiers	le I /*tags a	w =		/*tag= b /mod base= OTHER /not=	/Hore= "IAMKA labelled CHymral	A2.		2001WO-US018675.	2000US-0209927P. 2000US-0209928P. 2000US-0210091P.
RESULT 1 AAD25159/c ID AAD25159 stan XX	AAD25159; 12-MAR-2002	ıman NOV4 ge	uman; NOV4;	eurological;	oagulation d	ultiple scle	bronchitis; probe; ss.	Homo sapiens.	Key	modified_base		modified_base			WO200194416-A2	13-DEC-2001.	07-JUN-2001;	07-JUN-2000; 07-JUN-2000; 07-JUN-2000;

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2002US-0384543P.
22-APR-2002; 2
30-MAY-2002; 2
03-JUN-2002; 2
15-AUG-2002; 2
                                                         31-MAR-2003;
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                                                                                                                                                                                                                                                    The invention relates to isolated nucleic acids encoding polypeptides, designated NOVX polypeptides. The NOVX polypeptide and nucleic acid are useful for treating cardiomyopathy, atherosclerosis, diabetes or a disorder related to cell signal processing and metabolic pathway modulation. The NOVX polypeptide, nucleic acid and antibody are useful for treating or preventing a syndrome, e.g. various tissue/organ inflammation, muscular discasses, cagulation disorders, cancers (leukaemia, adenocarcinoma), multiple sclerosis, respiratory diseases, reproductive disorders, allergy, seizures, mental depression, epilepsy, gastro-intestinal diseases, bone disorders, nephrological disorders, urinary system disorders, immunological disorders, disease, dermatomyositis and bronchitis. The present sequence is a probe
                                                                                                                                                                       Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful for treating a syndrome associated with a NOVX-associated disorder, e.g. cardiomyopathy, atherosclerosis, neurological and neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer; chromosome mapping; human; probe; ss.
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                                                                                                     Colman SD, Padigaru M;
L, Malyankar UM, Gangolli E;
Ellerman K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26 BP; 8 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
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                                                                                                      Tchernev VT,
irgess C, Li
                                                                                                                 Burgess C, Li
, Smithson G,
                                                                                                                                                                                                                                  Example 1; Page 151; 189pp; English
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26-JUN-2000; 2000US-0214023P.
26-JUN-2000; 2000US-0214150P.
29-JUN-2000; 2000US-021500SP.
20-FEB-2001; 2001US-0270660P.
26-FEB-2001; 2001US-0271633P.
26-MAR-2001; 2001US-0271631P.
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05-APR-2002; 2002US-0370349P.
04-APR-2002; 2002US-0370569P.
12-APR-2002; 2002US-0372019P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-2003; 2003WO-US010142
                                                                                                                 B, Gusev V, B
Macdougall J,
                                                                                                      Majumder K, Spytek KA,
Zerhusen B, Gusev V, 1
                                                                                (CURA-) CURAGEN CORP.
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                                                                                                                   Zerhusen
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Mes; primer; PCR; human; immunoglobulin; Ig superfamily; BGS;
We aberrant immunoglobulin cell surface receptor activity;
We dellular adhesion disorder; hyper-immunoglobulin receptor activity;
Whypo-immunoglobulin receptor activity; aberrant signal transduction;
We reproductive disorder; female reproductive disorder; ovarian disorder;
We ovarian cancer; sexual dysfunction; infertility;
Welvic inflammatory disease; endometriosis; premature menopause;
We played inflammatory disease; endometriosis; premature menopause;
We becental dysfunction; hormone deficiency; oestrogen deficiency;
We berrant androgen metabolism; polycystic ovarian disease;
We aberrant androgen metabolism; polycystic ovarian disease;
We resistant-ovary syndrome; hermaphroditism; immunodeficiency;
We inflammatory disorder; arthritis, actime; immunodeficiency;
We active and arthritis; inflammatory bowel disease;
We active psoriasis; hypersensitivity; "c-cell mediated cytotoxicity;
We active anaemia; dematitis; glomerulonephritis; Graves' Disease;
We multiple sclerosis; myasthenia gravis; systemic lupus erythematosus;
We intuine dependent diabetes mellitus; autoimmune inflammatory eye disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NOVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromesome mapping. The present sequence is that of an oligonucleotide probe which was used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NOVX polypeptide, useful for preparing a composition for treating or preventing e.g. cancer or for chromosome mapping.
                                                                                                                                                                                                                                                                                                            Anderson DW, Bento P, Boldog FL, Burgess CE, Casman SJ, Furtak K; Gorman L, Gould-Rothberg BE, Gunther E, Heyes MP, L1 L, Spytek KA; Stone DJ, Zhong M, Malyankar UM, Edinger SR, Patturajan M; Rothenberg ME, Smithson G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26 BP; 8 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example C; SEQ ID NO 111; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CUGCAACUGAGAGGGGCUGGUU 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 CTGCAGCTGAGAGTGTCTGGTT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sjogren's disease; scleroderma
2002US-00160619.
2002US-0403748P.
2002US-00287226.
2003US-00403161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE03643 standard; DNA; 23 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-812539/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BGS PCR primer #27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention.
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99CN-00118819 99CN-00118819.

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Unidentified
                                                                                           07-SEP-1999;
                                                                                                                     07-SEP-1999;
                                       CN1287171-A.
                                                                  14-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                              and use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ29694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated mucleic acid molecule encoding BGS-
2, 3 and 4 polypeptides. The nucleic acid molecule, polypeptide and methods are useful for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant immunoglobulin cell sufface receptor activity; a callular adhesion disorder; a disorder related to hyper- or hypo-immunoglobulin receptor activity; a disorder related to berrant signal transduction; a reproductive disorder; an ovarian disorder; ovarian cancer; sexual female reproductive disorder; an ovarian disorder; ovarian cancer; sexual dysfunction; infertility; pelvic inflammatory disease; endometriosis; premature menopause; placental dysfunction; hormone deficiency; osetrogen deficiency; aberrant androgen metabolism; polycystic ovarian disease; aberrant ovarian cycle; dysfunctional uterine bleeding; realstant-ovary syndrome; hermaphroditism, immune disorders; inflammatory disorders; activities, asthma; immunodeficiency diseases uch as ADS; leuksemia; inflammatory bowel disease; sepsis; acne; psoriasis; hypersenstivity; such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues; or autoimmunity disorders; autoimmune infertility; Addison's Disease; haemolytic anaemia; rheumatoid arthritis; dermatitis; graves; disorders; bleaned; dispendent dispetes mellitus gravis; and tissues; or autoimmunity disorders; autoimmune infertility; dermatitis; graves; systemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                     New isolated nucleic acid molecule encoding BGS-2, 3 and 4 polypeptides, useful for preventing, treating or ameliorating a medical condition, e.g. a disorder related to aberrant immunoglobulin cell surface receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune inflammatory eye disease; Sjogren's disease; and sleroderma. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human neuronal calcium sensor protein 1 related oligonucleotide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.1%; Score 16.2; DB 10; Length 23; 38.1%; Pred. No. 4.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; neuronal calcium sensor protein 1; NCS-1; primer; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23 BP; 2 A; 4 C; 5 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                  Cheng JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.1%; Pred. ....
                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 228; 242pp; English
                                                                                                                                                                                                                  Feder JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 GCGCUUUGCUUCUGUUUUCUG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||||:::| :: :|::: |::| GCGCTTTGATTATGTTTCCTG 21
                                                               11-JUL-2002; 2002US-00193477
                                                                                          11-JUL-2001; 2001US-0304888P
12-APR-2002; 2002US-0372147P
                                                                                                                                                                                                                  Lee L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH74161 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                   WUS.
KRYSTEKSR.
                                                                                                                                                                                                                                             WPI; 2003-844480/78
                                                                                                                                                                         FEDER J N. CHENG J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                  Krystek SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention.
              US2003195163-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scleroderma.
                                       16-OCT-2003.
                                                                                                                                                                                                                                                                                                                activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH74161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                 (WUSS/)
                                                                                                                                                                                      CHEN/)
                                                                                                                                                              LEEL/)
                                                                                                                                                                         (FEDE/)
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1D AAH7416
XX
XX
DT 09-0CT
XX
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KW Human 1
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1. The present invention also relates to the protein, the application of the polynucleotide and the polypeptide, and the production process of the polynucleotide and the polypeptide
                                                                                                                                                                                                                                                                                                                The present invention provides the CDNA sequence of human neuronal calcium sensor protein 1 (NCS-1). The NCS-1 protein is a member of the neuronal calcium ion binding protein family and a homologue of human NCS-
                                                                                                                                                                        Human neuron calcium sensing protein and its code sequence, preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide B2del242-326 for domain deletion mutant of hbeta-2 GPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human beta-2 glycoprotein I; hbeta-2 GPI; beta-2 GPI domain 1; oligonucleotide B2del242-326; sushi domain; beta-2 GPI-dependent antiphospholipid antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linnik MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.1%; Score 16.2; DB 4; Length 29; 58.6%; Pred. No. 4.4e+04; ive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Victoria EJ, Jones DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29 BP; 6 A; 8 C; 7 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                        Example 4; Page 13 (Disclosure); 21pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 CUGAGAGGGCUGGUUAAGGCGUCCCCAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: || || || || || || CTACGACGGCTGGTATAGGAATTCCCAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ29694 standard; DNA; 30 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0088656P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0103088P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US013194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LJOL-) LA JOLLA PHARM CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 58.6
nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iverson GM,
                                                        Yu L, Fu Q, Zhao Y;
                                                                                                             WPI; 2001-398934/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-116542/10
UYFU-) UNIV FUDAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9964595-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-OCT-1998;
08-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marquis DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-DEC-1999.
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Gaps

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Indels

88.

RESULT 6 AED56453 ID AED50

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##X8X000000X8

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The invention relates to an oligonucleotide array (1) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (1) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid above method is useful for detecting a target nucleic acid with (1). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
                                                         Score 16.2; DB 14; Length 30; Pred. No. 4.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.8; DB 6; Length
Pred. No. 5.9e+04;
                Seguence 30 BP; 4 A; 3 C; 12 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide array; adapter sequence; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide adapter/capture probe 10993
                                                                                                       9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3, Mismatches
                                                                                                                                                   41 AAGUUGGAAGGCCCUUUGCUUCUGUUUU 69
                                                                                                                                                                          1 ACGITGGAIGAGGTGCTIIGCAGGIGITGI 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 225; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGAGGGCUGGUUAAGGC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВР.
                                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-AUG-2001; 2001WO-US026519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0227948P.
2000US-0228854P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.68;
                                                                                ilarity 41.4%;
Conservative
                                                              19.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ04674 standard; DNA; 24
                                                                                                                                                                                                                                                                                                        ABQ11002 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 73.7
les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·<del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ILLU-) ILLUMINA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-292068/33.
                                                                                Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200216649-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-AUG-2000;
29-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gunderson K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                                                                      ABQ11002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ04674
                                                              Query Match
                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                      ABQ11002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ04674
                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
χg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SXB
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                                                                                                                                                                                          셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                  The present sequence is oligonucleotide B2del242-326 used for generating domain deletion mutant of human beta-2 glycoprotein I. Isolated domain I of beta-2 GPI binds to and inhibits beta-2 GPI-dependent antiphospholipid antibodies. Amino acids 242-326 are deleted from beta-2 GPI and the resulting protein concains 1, 2, 3 and 4 sushi domains. This is used to determine the antigenic regions of beta-2 GPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of identifying a subject at risk of osteoarthritis which comprises detecting the presence or absence of one or more polymorphic variations associated with osteoarthritis in a nucleic acid sample where the presence of the polymorphism indicates a risk of osteoarthritis. The method is useful for identifying a subject at risk of osteoarthritis. The method is also useful for identifying a subject for treating osteoarthritis. The present sequence represents a PCR primer used to identify single nucleotide polymorphisms associated with osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a subject at risk of osteoarthritis comprises detecting the presence or absence of one or more specified polymorphic variations associated with osteoarthritis in a nucleic acid sample from a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Langdown ML;
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteoarthritis; musculoskeletal disease; Antiarthritic; Osteopathic;
RNAi; RNAi interference; ADAMTS2 agonist; ss; PCR; primer.
New isolated domain 1 beta-2 GPI polypeptides, used for inhibiting antiphospholipid antibodies for treating, e.g. thrombosis.
                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                   Score 16.2; DB 3; Length 30;
Pred. No. 4.5e+04;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reneland RH,
                                                                                                                                                                                                                                                               Sequence 30 BP; 6 A; 6 C; 11 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human osteoporosis related SNP primer #413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nelson MR,
                                                                                                                                                                                                                                                                                                                                                                                                                      :||: | || || || ||| ::|| || ||| || || rggrgarggcarggc30
                                                                                                                                                                                                                                                                                                                                                                                                 25 UGGUUAAGGCGUCCCCAAGUUGGAAGGGC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 88; 539pp; English.
                                                                Example 1; Page 51; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-2004; 2004US-0559011P.

01-APR-2004; 2004US-0559040P.

01-APR-2004; 2004US-0559042P.

01-APR-2004; 2004US-0559202P.

01-APR-2004; 2004US-0559203P.

01-APR-2004; 2004US-0559225P.
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                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.6%;
Matches 17; Conservative
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The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
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target nucleic acid sequence, has different addresses comprising
different specific capture probes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.8; DB 6; Length 24;
Pred. No. 5.9e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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                                                                                                                                                                                                        Claim 1; Page 147; 261pp; English
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29-AUG-2000; 2000US-0228854P.
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Best Local Similarity 73.7%;
Matches 14; Conservative
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                   (ILLU-) ILLUMINA INC.
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                                                                                         WPI; 2002-292068/33
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                                                      Gunderson K;
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                                                                                         Oligonucleotide array; adapter sequence; probe; ss.
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                                                    Oligonucleotide adapter/capture probe 4665.
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GAGAGGCGTTGGTTAAGGC 22
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2000US-0228854P.
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29-AUG-2000; 2000US-0228854P.
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                 (first entry)
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                   11-JUN-2002
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RESULT 12
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nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ1409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (1). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid.
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Pred. No. 5.9e+04;
3; Mismatches 2; Indels
                                                                                                                                                                                                        Score 15.8; DB 6; Length 24; Pred. No. 5.9e+04;
                                                                                                                                                                                                                                                         2; Indels
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                                                                                                                                                      Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                         3; Mismatches
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29-AUG-2000; 2000US-0228854P
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Best Local Similarity 73.7%;
Matches 14; Conservative
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Best Local Similarity
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Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
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                                                                                                                                                        Oligonucleotide adapter/capture probe 12529
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29-AUG-2000; 2000US-0228854P.
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ABQ12538 standard; DNA; 25
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Best Local Similarity 40.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOC145197.
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roth RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
ADY03184
  CCCCXSXLLLXBXBXXBXBXXBXXXXXXXXXXXXXCCCCCXXSXXBXXBXXBXXBXXBXXBX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an oligonucleotide array (I) comprising at least different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in AB000010-AB013409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (AB000010-AB013409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid.
                                                                                                                                                                                                                                              or detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                         Array comprising adapter sequences useful for immobilizing or de target nucleic acid sequence, has different addresses comprising different specific capture probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.8; DB 6; Length 25;
Pred. No. 6e+04;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reneland R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 BP; 5 A; 10 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer 156 used to amplify human DPF3 SNP DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP detection, breast tumor, endocrine disease, gynecology and obsterrics, neoplasm; cytostatic; gene therapy; NNA interference; ss; PCR; primer; D4, zinc and double PHD fingers, family 3; DPP3; guanine-nucleotide exchange factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kammerer SM,
                                                                                                                                                                                                                                                                                                                               Claim 1; Page 244; 261pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 GAGAGGGCUGGUUAAGGC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 GAGAGGCGTTGGTTAAGGC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Braun A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUL-2003; 2003US-0490234P.
25-NOV-2003; 2003US-00723681.
25-NOV-2003; 2003US-0525239P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.6%;
                   27-AUG-2001; 2001WO-US026519
                                                         25-AUG-2000; 2000US-0227948P
29-AUG-2000; 2000US-0228854P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAY-2004; 2004WO-US016939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADY01452 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAY-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                        (ILLU-) ILLUMINA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SEQU-) SEQUENOM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nelson MR,
                                                                                                                                                                                                     WPI; 2002-292068/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-163257/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoyal-Wrightson CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2005014846-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                Gunderson K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-FEB-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roth RB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
ADY01452
LD ADY01452
AC ADX01
XX ADX01
XX ADX01
XX ADX01
XX SNP
XM SYNE
XM SYNE
XM SQUAN
XX BQL
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel method for identifying a subject at risk of breast cancer comprising detecting the presence or absence of a polymorphic variation associated with breast cancer. The method of the invention demonstrates cytostatic activity and may be useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP detection; breast tumor; endocrine disease; gynecology and obstetrics; neoplasm; cytostatic; metastasis; gene therapy; RNA interference; ds; SNP; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Identifying risk of, preventing and/or treating breast cancer by identifying and/or analyzing polymorphic variations in nucleotide sequences within the human genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying risk of, preventing and/or treating breast cancer by identifying and/or analyzing polymorphic variations in nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.4%; Score 15.6; DB 14; Length 30; 40.0%; Pred. No. 7.6e+04; Live 9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reneland R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primer 7 used to amplify human LOC145197 SNP DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30 BP; 5 A; 7 C; 7 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kammerer SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AAGUUGGAAGGCGCUUUGCUUCUGUUUUC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACGTTGGATGGGTCACATACTTCTGTCTTC 30
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                                                                                                                                                                                 Example 16; Page 239; 617pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences within the human genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nelson MR, Braun A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-2003; 2003US-0490234P.
25-NOV-2003; 2003US-00723681.
25-NOV-2003; 2003US-0525239P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAY-2004; 2004WO-US016939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADY03184 standard; DNA; 30
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CC identifying a risk of, preventing and/or treating breast cancer and CC cancer metastasis. The methods may be utilized for gene therapy or RNA CC interference. The current sequence is that of a PCR primer of the CC interference. The current sequence is that of a PCR primer of the CC intention which was used to amplify a human LOC145197 DNA containing a XX Squence 30 BP; 5 A; 7 C; 8 G; 10 T; 0 U; 0 Other; Squence 30 BP; 5 A; 7 C; 8 G; 10 T; 0 U; 0 Other; Query Match 18.4%; Score 15.6; DB 14; Length 30; Best Local Similarity 43.3%; Pred. No. 7.6e+04; Matches 13; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
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8 8

Search completed: October 16, 2006, 14:15:59 Job time : 446.812 secs

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; ORGANISM: Mus musculus US-10-719-900-385230
US-10-719-900-385230
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                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                         Published Applications NA Main:*

1: /EMC Celerra_SIDS3/prodata/2/pubpna/US07_PUBCONB.seq:*
2: /EMC_Celerra_SIDS3/prodata/2/pubpna/US08_PUBCONB.seq:*
3: /EMC_Celerra_SIDS3/prodata/2/pubpna/US09A_PUBCONB.seq:*
4: /EMC_Celerra_SIDS3/prodata/2/pubpna/US09B_PUBCONB.seq:*
5: /EMC_Celerra_SIDS3/prodata/2/pubpna/US09B_PUBCONB.seq:*
6: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10A_PUBCONB.seq:*
7: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10B_PUBCONB.seq:*
8: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10B_PUBCONB.seq:*
10: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10B_PUBCONB.seq:*
11: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10B_PUBCONB.seq:*
12: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10F_PUBCONB.seq:*
13: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10F_PUBCONB.seq:*
14: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11A_PUBCONB.seq:*
14: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11A_PUBCONB.seq:*
14: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11A_PUBCONB.seq:*
14: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11A_PUBCONB.seq:*
15: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11A_PUBCONB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 172709,
Sequence 111, App
Sequence 13212,
Sequence 13212, A
Sequence 13212, A
Sequence 292691,
Sequence 292693,
Sequence 38695,
Sequence 386965,
Sequence 386965,
Sequence 386965,
Sequence 386965,
Sequence 386966,
Sequence 776242,
Sequence 888593,
                                                                              October 16, 2006, 14:16:09 ; Search time 1197.03 Seconds (without alignments) 872.534 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 385230,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 453865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                      1 ggguuaucugcaacugagag........
           GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-719-900-453865

US-10-933-982-172709

US-10-403-161-111

US-10-310-914A-166755

US-10-750-185-13212

US-10-750-623-13212

US-10-750-623-13212

US-10-310-914A-106490

US-10-310-914A-106490

US-11-121-849-38693

S US-11-121-849-38695

US-11-121-849-386965

US-10-719-900-888593

US-10-719-900-888593

US-10-719-900-888593
                                                                                                                                                                                                             18892170 segs, 6143817638 residues
                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        - nucleic search, using sw model
                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                            US-10-604-726A-6033
85
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Match Length DB
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                                                                                                                             Title:
Perfect score:
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TYPE: RNA
ORGANISM: Human
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sequence 111, Application US/10403161

publication No. US20040043930A1

General INFORMATION:

APPLICANT: Anderson, David et al.

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

TITLE OF INVENTION: David et al.

CURRENT APPLICATION NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

CURRENT FILING DATE: 2003-03-31

PRIOR APPLICATION NUMBER: 60/370349

PRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2002-04-08

PRIOR FILING DATE: 2002-04-08

PRIOR FILING DATE: 2002-04-15

PRIOR PELICATION NUMBER: 60/372019

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2000-02-08

PRIOR FILING DATE: 2000-02-08

PRIOR FILING DATE: 2000-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08
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; Publication No. US20060051769A1
; GENERAL INFORMATION:
    APPLICANT: Barts, Jennifer
; TITLE OF INVENTION: Methods of Genetic Analysis of E. coli
    FILE REFERENCE: 3700
; CURRENT APPLICATION NUMBER: US/10/933,982
; CURRENT FILING DATE: 2004-09-03
; NUMBER OF SEQ ID NOS: 224976
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 172709
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 25;
                                                                                                                                                                                                                                                                                 21.4%; Score 18.2; DB 9; Length 25; 69.6%; Pred. No. 1.4e+04; Live 4; Mismatches 3; Indels
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 453865
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 21.4%; Score 18.2; DB 11; Best Local Similarity 47.8%; Pred. No. 1.4e+04; Matches 11; Conservative 9; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                 35 GUCCCCAAGUUGGAAGGGCGCUU 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACCCCAAGTTGGAAGGCGGCTT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 AAGGCCCUUUGCUUCUGUUUUC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 AACGCCCTTTACCTCTGTTTTC 3
                                                                                                                                                                                                                                                                                                                 Best Local Similarity 69.6
Matches 16; Conservative
                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-453865
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US-10-933-982-172709/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: E. coli
US-10-933-982-172709
                                                                                                                                                                                                                                                                                          Query Match
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Sequence 166755, Application US/10310914A

Fublication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Wusat
APPLICANTON: uses thereof
TITLE OF INVENTION: uses thereof
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 166755
LENGTH: 27
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PRIOR APPLICATION NUMBER: 60/262892
PRIOR FILING DATE: 2001-01-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 173
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 111
LENGTH: 26
                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: Description of Artifical Sequence: Primer/Probe US-10-403-161-111
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Sequence 13212, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.

APPLICANT: MAI GENOMICS, INC.

APPLICANT: RERR Richard

APPLICANT: ROSENFELD, David

APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTINN: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MAILINO-2

CURRENT PILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR PILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SEQ ID NO 12212

LENGTH: 24

LENGTH: 24
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21.4%; Score 18.2; DB 8;
Best Local Similarity 65.2%; Pred. No. 1.4e+04;
Matches 15; Conservative 5; Mismatches 3;
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26 GGTCCCTTTGCTTCTGGTTTCTG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:||| |:|||| |:||::|
23 CTGCAGCTGAGAGTGTCTGGTTA 1
                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 43.5%
Matches 10; Conservative
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Sequence 292693
Sequence 292693
Sequence 292693, Application US/11121849
Sequence 292693, Application US/11121849
Sequence 292693, Application US/11121849
Sequence 292693, Application US/20050272080A1
Sequence 292693
TUTLE OF UNIVERTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Se
TITLE OF INVENTION: Microarrays
FILE OF INVENTION: Microarrays
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SEQ ID NOS: 673904
SEQ ID NO 292693
LENGTH: 25
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                                                                                                                                                                                                                                                                            Sequence 113202, Application US/11036317

Sequence 113202, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITIE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SEQ ID NO 713202

LENGTH: 25
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Pred. No. 2.3e+04;
4; Mismatches 4;
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41.7%; Pred. No. 2.3e+04;
iive 10; Mismatches 4;
Best Local Similarity 45.8%; Pred. No. 2.3e+04; Matches 11; Conservative 9; Mismatches 4
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                                                                                      50 GGGCGCUUUGCUCUGUUUCUGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 GAGAGGGCUGGUUAAGGCGUCCC 39
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Best Local Similarity 41.74
Matches 10; Conservative
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Best Local Similarity 66.7
Matches 16; Conservative
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; ORGANISM: Mus musculus
US-11-036-317-713202
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US-11-121-849-292693
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US-11-121-849-386034/c
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Sequence 106490, Application US/10310914A
Sequence 106490, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION: Beac
APPLICANT: Shiler, Kvuzat
APPLICANT: Biller, Kvuzat
APPLICANT: Biller, Kvuzat
APPLICANT: Shiler, Mvizat
APPLICANT: Shiler
APPLICA
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; Sequence 13212, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INPORMATION:
; APPLICANT: MI GENOMICS, INC.
; APPLICANT: ROSENFELD, David
; APPLICANT: ROSENFELD, David
; APPLICANT: RATES, Stephen
; APPLICANT: FAMTH, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT PILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN Version 3.1
; SEQ ID NO 13212
; LENTH: 24
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                                                                                                                                                                             20.9%; Score 17.8; DB 10; Length 24; 38.1%; Pred. No. 2e+04; tive 11; Mismatches 2; Indels
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2e+04;
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2e+04;
ches 2;
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                                                                                                                                                                                                                                                                                                                                 1 TTTACATCTGTTTTCTGGATG 21
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; OTHER INFORMATION: Reverse Primer
US-10-750-185-13212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: Reverse Primer US-10-750-623-13212
TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial sequence
                                                                                                                                                                                Query Match
Best Local Similarity 38.1%
Matches 8; Conservative
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Best Local Similarity 38.1%
Best Local 8; Conservative
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; ORGANISM: Human
US-10-310-914A-106490
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Gape

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RESULT 14
US-11-121-089-386566/c
US-11-121-080-05

Sequence 386966, Application US/11121849

Sequence 386966, Application US/11121849

Publication No. US2000272080A1

GENERAL INFORMATION:
APPLICATION
MICTOART: John Palma
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2004-05-03

PRIOR PILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Uses thereof
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 776242
LENGTH: 24
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                                                                                         Score 17.6; DB 15;
Pred. No. 2.3e+04;
5; Mismatches 4;
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                                                                                                                                                                                                                             8 CUGCAACUGAGAGGGGCUGGUUAA 31
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                                                                                               Query Match 20.7%;
Best Local Similarity 62.5%;
Matches 15; Conservative
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ORGANISM: Homo sapien
      ; ORGANISM: Homo sapien
US-11-121-849-386965
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US-10-310-914A-776242/c
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US-10-310-914A-776242
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US-11-121-849-386965/c
; Sequence 386965, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; AFPLICANT: John Palma
; TITLE OF INVENTION: Microarray8
; FILE REFERENCE: 3684.1
; FILE REFERENCE: 3684.1
; FILE REFERENCE: 3684.1
; FILE NOTE TAIL OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 386035, Application US/11121849
; Publication No. US20050272080A1
; Publication No. US20050272080A1
; GENERAL INPORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Microarray9
; TITLE OF INVENTION: Microarray9
; TITLE OF INVENTION WINBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR RILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded STITLE OF INVENTION: Microarrays
FILE REPERBNCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 00/567,949
PRIOR PLING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Mcroarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 386034
LENGTH: 25
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Pred. No. 2.3e+04;
5; Mismatches 4;
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US-11-121-849-386035
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US-11-121-849-386034
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US-11-121-849-386035/c
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1052105,
17, Appl
                                                                                                                             October 16, 2006, 14:16:55; Search time 188.534 Seconds (without alignments) 842.395 Million cell updates/sec
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| EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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Match Length
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Perfect score:
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Sequence 435988, Application US/11348413

Sequence 435988, Application US/11348413

Publication No. US20060160121A1

GENERAL INFORMATION:

APPLICANT: Wyels

APPLICANT: Murphy, Ellen

APPLICANT: Murphy, Ellen

APPLICANT: OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES

FILE REFERENCE: 031896-084100 (AM 101724)

CURRENT PILING DATE: 2006-02-07

PRIOR APPLICATION NUMBER: US/11/348,413

CURRENT PILING DATE: 2005-10-05

PRIOR PILING DATE: 2005-10-05

PRIOR PILING DATE: 2005-10-05

PRIOR PILING DATE: 2005-10-05

PRIOR PILING DATE: 2004-10-05

NUMBER OF SEQ ID NOS: 1276209

SEQ ID NO 835988

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13247, A
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7, Appli
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; OTHER INFORMATION: SEQ ID NO: 6556; WANOLUKVS_at; Start 526; Stop 550;
; OTHER INFORMATION: 00000011100000
US-11-348-413-835988
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40.0%; Pred. No. 6.3e+03;
ive 10; Mismatches 5; Indels
                         US-11-217-529-152213
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US-11-348-413-26155
US-11-348-413-661513
US-11-348-413-669513
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US-11-217-529-96809/c
Sequence 96809, Application US/11217529
; Publication No. US20060099612A1
 Best Local Similarity 40.03
Matches 10; Conservative
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US-11-348-413-835988
Query Match
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Sequence 98397, Application US/11217529 Publication No. US20060099612A1 GENERAL INFORMATION: APPLICANT: SUNTORY LIMITED
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Best Local Similarity 33.34
Matches 7; Conservative
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Matches 15; Conserv
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; Sequence 183005, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
    APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAWURA, NORIHISA
; APPLICANT: NAKAWURA, TOWNINKO
; APPLICANT: FUJIWURA, TOWNINKO
; APPLICANT: FUJIWURA, TOWNINKO
; APPLICANT: FUJIWURA, TOWNINKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT APPLICATION NUMBER: US 10/932,182
; PRIOR APPLICATION NUMBER: US 10/932,182
; RUDMABER OF SEQ ID NOS: 197023
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
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                                          APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: KUJMURA, TOMOKO
APPLICANT: ASHIKANT TOSHIHIKO
APPLICANT: ASHIKANT YOSHIHIKO
APPLICANT: ASHIKANT YOSHIHIKO
APPLICANTON: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR PAPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
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19.5%; Score 16.6; DB 8; Length 25;
Best Local Similarity 60.9%; Pred. No. 8.9e+03;
Matches 14; Conservative 5; Mismatches 4; Indels
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19.3%; Score 16.4; DB 8; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 9; Conservative 8; Mismatches 1; Indels
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Publication No. US20060160121A1
FEBRAL INFORMATION:
APPLICANT: Worth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmeted, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 UCCCCAAGUUGGAAGGGCGCUUU 58
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Saccharomyces pastorianus US-11-217-529-96809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 TTCCCAATTGTGAAGGCCCTTT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Saccharomyces pastorianus US-11-217-529-183005
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                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 96809
LENGTH: 25
APPLICANT: SUNTORY LIMITED APPLICANT: NAKAO, YOSHIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-11-348-413-960036/c
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LENGTH: 25
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TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES FILE REFERENCE: 031896-084100 (AM 101724)

CURRENT APPLICATION NUMBER: US/11/348,413

CURRENT FILING DATE: 2006-02-07

PRIOR PELICATION NUMBER: PCT/USOS/035471

PRIOR FILING DATE: 2005-10-05

PRIOR FILING DATE: 2005-10-05

PRIOR PELICATION NUMBER: US 60/615,573

PRIOR FILING DATE: 2005-10-05

PRIOR FILING DATE: 2006-10-05

PRIOR FILING DATE: 2004-10-05

NUMBER OF SEQ ID NOS: 1276209

SEQ ID NO 96036
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; Publication No. US20060099612A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, TOMOKO
APPLICANT: KODAWA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA: US/11/217,529
CURRENT FILING DATE: 2006-09-02
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PALENTIN VERSION 3.3
SEQ ID NO 52650
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
SGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(25)
OTHER INFORMATION: SEQ ID NO: 10014; WANOIFG3J_at; Start 207; Stop 231;
OTHER INFORMATION: 00000000100000
US-11-348-413-960036
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ilarity 62.5%; Pred. No. 1.5e+04;
Conservative 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.1%; Score 16.2; DB 9; 33.3%; Pred. No. 1.3e+04;
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Sequence 411718, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                                         ORGANISM: Saccharomyces pastorianus US-11-217-529-94477
                                                                                                                                                                                                                                                                                                                                                                                                                           47 GAAGGCGCUUUGCUUCUGUUU 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-99137
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-217-529-99137
                                                                                                                                                                                                                                         TYPE: DNA
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Sequence 29948, Application US/11217529

Publication No. US20060099612A1

GENERAL INFORMATION:

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: ASHIKARI, TOSHIHIRO

APPLICANT: ASHIKARI, TOSHIHIRO

TITLE REFERENCE: S-38-285

CURRENT APPLICATION NUMBER: US/11/217,529

CURRENT FILING DATE: 2005-09-02

PRIOR FILING DATE: 2004-09-02
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAWURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIWURA, TOWKO
APPLICANT: RUNENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
FRIOR PILING DATE: 2005-09-02
FRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ 1D NOS: 127023
SOFTMARE: PATENTIN NOS: 127023
SOFTMARE: PATENTIN VERSION 3.3
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18.4%; Score 15.6; DB 8;
Best Local Similarity 45.5%; Pred. No. 2.1e+04;
Matches 10; Conservative 8; Mismatches 4;
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Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SINTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAOWRA, NORIHISA
APPLICANT: NAKAOWRA, YUKIKO
APPLICANT: FUJIMURA, TOWOKO
APPLICANT: FUJIMURA, TOWOKO
APPLICANT: ASHIKARI, TOSHIHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Saccharomyces pastorianus US-11-217-529-29948
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GCTTTGCTTCTGGTTTATG 22
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SOFTWARE: Patentin version 3.3
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Best Local Similarity 36.00
Best Local 7; Conservative
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LENGTH: 25
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APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INTENT. Olmsted, Stephen
TITLE OF INTENT. Olmsted, Stephen
TITLE OF STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
PRIOR APPLICATION NUMBER: PCT/USO5/035471
PRIOR APPLICATION NUMBER: US/123,445
PRIOR PLING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
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Sequence 99137, Application US/11217529

Publication No. US20060099612A1

GENERRAL INFORMATION:

APPLICANT: SUNTORY LIMITED

APPLICANT: NAKAWIRA, NORIHISA

APPLICANT: NORAWIRA, TUKIKO

APPLICANT: KODAMA, TUKIKO

APPLICANT: WINDERTION: METHING FOR ANALYZING GENES OF INDUSTRIAL YEASTS

TILLE OF INVENTION: METHINGS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: S-38-285

CURRENT APPLICATION NUMBER: US/11/217, S29

CURRENT APPLICATION NUMBER: US 10/932, 182

PRIOR APPLICATION NUMBER: US 10/932, 182

PRIOR PLING DATE: 2004-09-02.

NUMBER OF SEQ ID NOS: 197023

SEQ ID NO 99137

LENGTH: 25
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TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
RIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 94477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
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APPLICANT: Mounte, William M
APPLICANT: Mounted, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olimpted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REPERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT PILING DATE: 2006-02-07
RRIOR APPLICATION NUMBER: PCT/US05/035471
RRIOR APPLICATION NUMBER: US 11/243,445
RRIOR APPLICATION NUMBER: US 11/243,445
RRIOR APPLICATION NUMBER: US 60/615,573
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR PILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NOS: 1276209
                                       APPLICANT: MULPHY, Ellen
APPLICANT: MULPHY, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REPRERNCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
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LOCATION: (1): (25)
OTHER INDORNATION: SEQ ID NO: 7816; WANOIUMPL_at; Start 185; Stop 209;
OTHER INFORMATION: 000000010000000
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NAME/KRY: misc feature
LOCATION: (1). 7(25)
OTHER INFORMATION: SEQ ID NO: 12552; WANOIUOO2; Start 495; Stop 519;
OTHER INFORMATION: 00000000011111
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18.4%; Score 15.6; DB 9;
Best Local Similarity 36.4%; Pred. No. 2.1e+04;
Matches 8; Conservative 10; Mismatches 4;
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                       Mounts, William M
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Best Local Similarity 36.44
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial
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APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TILLE APPLICANT: Olmsted, Stephen
TILLE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-10-05
PRIOR APPLICATION NUMBER: PCT/USOS/035471
PRIOR APPLICATION NUMBER: PCT/USOS/035471
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2005-10-05
PRIOR PLING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 414079
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                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: (1). (25)
; OTHER INFORMATION: SEQ ID NO: 12488; WANOIUOM6; Start 38; Stop 62;
; OTHER INFORMATION: 00000000011110
US-11-348-413-411718
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Best Local Similarity 36.4%; Pred. No. 2.1e+04;
Matches 8; Conservative 10; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   18.4%; Score 15.6; DB 9; 36.4%; Pred. No. 2.1e+04; tive 10; Mismatches 4;
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 411718
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 414079, Application US/11348413; Publication No. US20060160121A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 414080, Application US/11348413; Publication No. US20060160121A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 GCUUUGCUUCUGUUUUCUGGAU 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 GCUUUGCUUCUGUUUUCUGGAU 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 GGTGTGGTTCTGTATTCTGGAT 4
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Matches 8; Conservative
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US-11-348-413-414079/c
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US-11-348-413-414080/c
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                                                                                                                                                         TYPE: DNA
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAORA, VORIHISA
APPLICANT: NAKAORA, VORIHISA
APPLICANT: NAKAORA, VORIHISA
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT APPLICATION NUMBER: US 10/932,182
PRIOR PILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
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; LOCATION: (1). (25)
; OTHER INFORMATION: SEQ ID NO: 10828; WAN01UOXH; Start 36; Stop 60;
; OTHER INFORMATION: 00000000011101
US-11-348-413-350690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 18.1%; Score 15.4; DB 8; Length 25; Best Local Similarity 52.0%; Pred. No. 2.5e+04; Matches 13; Conservative 6; Mismatches 6; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 CUUCUGUUUUCUGGAUGCAGAGUCC 84
                                                                                                                                                                                                                                                                                                                    Sequence 98618, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
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ORGANISM: Saccharomyces pastorianus US-11-217-529-98618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: probe
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US-11-348-413-350690/c
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  Length 25;
Query Match 18.1%; Score 15.4; DB 9; Best Local Similarity 40.0%; Pred. No. 2.5e+04; Matches 10; Conservative 9; Mismatches 6;
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Search completed: October 16, 2006, 14:22:02 Job time : 189.534 secs

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nucleic

Run on:

Sequence:

Minimum DB Maximum DB

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Result

Searched:

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AC141634 CACNAID B
AC141632 CACNAID t
AC143064 CACNAID B
AC457579 Human ost
Abg79069 Rat ZAO r
Abl5068 Rat G pro
Ad669148 Angiogene
Aa95201 Otoferlin
Aea25301 Anti-myos
                                                                                                Abz99113 Human PDE
Abd3214 Human PDE
Adj6098 Oligonucl
Ado46487 Human oli
Ad297886 Human ant
Aed42052 Ant18ense
Ad13385 Human BNA
Adu43508 Knock-dow
Ack10389 Human mic
Ack10389 Human mic
Accior human deb
Accior human deb
Accior human deb
Accior human deb
Accior turning
Adcior human deb
Accior human deb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Array comprising adapter sequences useful for immobilizing or detecting target nucleic acid sequence, has different addresses comprising different specific capture probes.
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                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide adapter/capture probe 10993
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                                                                                                                                                                                                ADD64634
ADO61007
AEC90171
ADZ15690
ADZ15691
ADW95301
AAQ89038
                                                           ADD69148
AAS95201
AEA25301
AEA25458
  ACL41634
ACL41632
ACL43064
AED57579
                                                                                                  ABZ99113
ABD32144
ABD32144
ADO46487
ADZ97886
ABD42052
ADJ13385
ADJ13385
ADJ13385
ADY43508
ARF85432
ACK10389
                                         ABQ79069
ABL50688
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29-AUG-2000; 2000US-0228854P.
    ABQ11002 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-292068/33.
   WO200216649-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
   ABQ11002;
    0 0 0 0 0 0 0 0 0 0 0 0 0 0
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Abg04715 Oligonucl
Abg10038 Oligonucl
Abg11043 Oligonucl
Abg12538 Oligonucl
Abg12579 Oligonucl
Aar74315 PCR prime
Aar74315 PCR prime
Aar74315 PCR prime
Aar743454 Manan CAB
Ada27885 Human ant
Adi33347 Human nhA
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Acd82777 Human mic
Acd57816 HCV DNAzy
Ad183268 HCV DNAzy
Aar47817 PCR prime
Aax04299 Mouse neu
                                                                     time 125.594 Seconds
alignments)
Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
             GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                    4443654
                                                                                (without 1332.341 P
                                                                      ; Search
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                               5244920 segs, 3486124231 residues
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Maximum Match 100%
Listing first 45 summaries
                                                  nucleic search, using sw model
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ABQ04115
ABQ01058
ABQ11043
ABQ12538
ABQ12579
AAT74115
AAL50117
ADZ27868
ADZ27864
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ACI82777
ACD57816
ADI83268
AAT47817
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Gapop 10.0 , Gapext 1.0
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geneseqn2003ds:*
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24
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Match
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Perfect score:
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2000US-0227948P. 2000US-0228854P.

ВР.

(first entry)

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Oligonucleotide array; adapter sequence; probe;
                                                                                  Oligonucleotide adapter/capture probe 4706
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  ABQ04715 standard; DNA; 24
                                                                                                                                                                                                                                                                                        (ILLU-) ILLUMINA INC.
                                                                                                                                                                                                                                                                                                                                          WPI; 2002-292068/33.
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29-AUG-2000;
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                                                     11-JUN-2002
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                                                                                                                                      Synthetic.
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                             ABQ04715;
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and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising
                                                                                                           Gaps
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                                                                               Query Match 65.8%; Score 15.8; DB 6; Length 24; Best Local Similarity 73.7%; Pred. No. 1.3e+03; Matches 14; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 65.8%; Score 15.8; DB 6; Length 24; Best Local Similarity 73.7%; Pred. No. 1.3e+03; Matches 14; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                             Oligonucleotide array; adapter sequence; probe; ss.
                                                       Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                  Oligonucleotide adapter/capture probe 4665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      target nucleic acid sequence, has different specific capture probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 147; 261pp; English
                                                                                                                                      2 GAGAGGGCUGGUUAAGGC 20
                                                                                                                                                                4 GAGAGGCGTTGGTTAAGGC 22
                                                                                                                                                                                                                                  ABQ04674 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-2001; 2001WO-US026519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-AUG-2000; 2000US-0227948P
29-AUG-2000; 2000US-0228854P
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Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
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Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide array; adapter sequence; probe; ss.
                                                                                                                                                                                                                                                                                                                                                  Seguence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide adapter/capture probe 349
                                                                                         Claim 1; Page 147; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GAGAGGGCUGGUUAAGGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٣
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 GAGAGGCGTTGGTTAAGGC
                                                                                                                                                                                                                                                                                                                                                                                          65.8%;
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GAGAGGCGTTGGTTAAGGC 22 

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RESULT 3 ABQ04715/c

Gaps

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Length 24; Indels

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25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
                                                                                                                                                         Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                       Score 15.8; DB 6;
Pred. No. 1.3e+03;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide array; adapter sequence; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide adapter/capture probe 12529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 244; 261pp; English.
                                                                                                                                                                                                                                                          2 GAGAGGGCUGGUUAAGGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 gagagggggggggg 20
                                                                                                                                                                                                                                                                              21 GAGAGGCGTTGGTTAAGGC 3
                                                                                                                                                                                                                                                                                                                                                                                 BP
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29-AUG-2000; 2000US-0228854P.
                                                                                                                                                                                       Query Match 65.8%;
Best Local Similarity 73.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 ABQ12538 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ12538;
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                                                                                                                                                                                                                                                                         The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABO00010-ABO13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABO00010-ABO13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
                                                                                                                                                                       Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an oligonucleotide array (I) comprising at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Array comprising adapter sequences useful for immobilizing or detecting target nucleic acid sequence, has different addresses comprising different specific capture probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide array; adapter sequence; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide adapter/capture probe 11034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 225; 261pp; English
                                                                                                                                                                                                                                            Claim 1; Page 52; 261pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GAGAGGGCUGGUUAAGGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GAGAGGCGTTGGTTAAGGC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABQ11043 standard; DNA; 24 BP
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29-AUG-2000; 2000US-0228854P.
                      25-AUG-2000; 2000US-0227948P
29-AUG-2000; 2000US-0228854P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                        (ILLU-) ILLUMINA INC
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                                                                                                          Gunderson K;
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25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) a useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
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         detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Array comprising adapter sequences useful for immobilizing or del target nucleic acid sequence, has different addresses comprising different specific capture probes.
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65.8%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. No. 1.3e+03;
Matches 14; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 7 A; 2 C; 10 G; 6 T; 0 U; 0 Other;
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Corynascus heterothallicus.
                                                                    29-JAN-1997;
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                            WO9728243-A1
                                                 07-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL50117;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                              Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cleaning; bleaching; cellulose; fabric; enzyme hybrid; peroxidase; cellulose binding domain; Humicola insolens; cellulase; Coprinus cinereus; laccase; plasmid pJC25; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 73.7%; Pred. No. 1.3e+03;
Matches 14; Conservative 3; Mismatches 2; Indels
                                                                                                                                   Oligonucleotide array; adapter sequence; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 5 A; 10 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                               Oligonucleotide adapter/capture probe 12570.
                                                                                                                                                                                                                                                                                                                                          target nucleic acid sequence, has different specific capture probes.
                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 244; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GAGAGGGCUGGUUAAGGC 20
 5 GAGAGGCGTTGGTTAAGGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 GAGAGGGTTGGTTAAGGC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT74315 standard; DNA; 28 BP
                                                                                                                                                                                                                   27-AUG-2001; 2001WO-US026519
                                                                                                                                                                                                                                     25-AUG-2000; 2000US-0227948P
29-AUG-2000; 2000US-0228854P
                                                 ABQ12579 standard; DNA; 25
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                                                                                          11-JUN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer JC25.2.
                                                                                                                                                                          WO200216649-A2
                                                                                                                                                                                                                                                                                         Gunderson K;
                                                                                                                                                                                              28-FEB-2002
                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT74315;
                                                                       ABQ12579;
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PCR primers CiPpcrdwn (AAT74310) and JC25.2 (AAT74315) were used to amplify a DNA fragment encoding the entire laccase protein (residues 1-620) of Myceliophthora thermophila plus 232 bp of upstream sequence, using plasmid pJRRoC30 as template. The PCR product was ligated to a DNA fragment encoding the Humicola insolens family 45 cellulase linker domain (35 amino acids), the H. insolens family 45 cellulase cellulose binding domain (CBD, 37 amino acids) plus 20 bp of 3'-noncoding sequences in vector pJC106 to obtain plasmid pJC35 (see AAT74282). A claimed process for removal or bleaching of soiling or stains on a cellulosic fabric comprises contacting the fabric with a modified enzyme (hybrid) comprising a catalytically active portion of a non-cellulolytic enzyme linked to a CBD. The hybrid enzyme gives improved enzyme performance by increasing the affinity of the enzyme for the fabric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Cleaning of cellulosic fabrics - using an enzyme hybrid comprising sequence of a non-cellulolytic enzyme linked to a cellulose-binding
                                                                                                                                                                                                                                                   Von Der Osten C, Cherry JR, Bjornvad M, Vind J, Rasmussen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.3%; Score 15.2; DB 2; Length 28; 75.0%; Pred. No. 2.5e+03; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human CAB55953-1 ligand binding domain PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28 BP; 3 A; 15 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 85; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GAGAGGGCUGGUUAAGGCG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 GCGAGTGGCTGGTCAAGGCG 1
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97WO-DK000042.
                                                                                 96DK-00000094
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nes 15; Conservative
                                                                                                                                                                      (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                        WPI; 1997-402598/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain sequence.
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The present invention describes a method for testing the presence or absence of a specific substance in a food by performing PCR with primers which are designed on the basis of data obtained from a part of a gene of the specific substance. Also described: (1) a similar method for detecting a trace component contained in a food, or for identifying a harful allergen specific to a consumer of such substance by performing PCR with primers which are designed on the basis of data obtained from a part of a gene of the specific substance; (2) primers for PCR applicable in food testing which are designed on the basis of data obtained from a part of a gene of the specific substance; and (3) kits for determining concentration of a specific substance in the food containing the primers. The methods are useful for testing foods, which can be used in detecting trace components or identifying specific harmful allergens in (processed) foods, particularly applicable in food safety and management. The present allergenic storage protein designated FAGAGI, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                PCR-based method for testing foods using specific primers designed from genes of target substance, useful in detecting trace components or identifying specific harmful allergens in (processed) foods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.0%; Score 14.4; DB 9; 68.8%; Pred. No. 5.9e+03;
                                                                                                                               Suzuki E, Miyatake K, Hayakawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein interaction; antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human antisense oligonucleotide SEQ ID NO:39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                     Disclosure, Page 10, 38pp; Japanese.
                                                                                     (NISS ) NISSHIN SEIFUN GROUP INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0256986P.
2001US-0259571P.
2001US-0259572P.
  26-SEP-2002; 2002WO-JP009982
                                          15-FEB-2002; 2002JP-00038930
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2000US-0185056P.
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2000US-0255063P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 GGCUGGUUAAGGCGU 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 GGCTGGTTATGGCGT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADZ97885 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                      WPI; 2003-637145/60.
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04-JAN-2001;
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                                                                                                                               Yamakawa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADZ97885/c
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BBBBBBAKLAXBXSXXXXBXLAXB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                 human nuclear hormone receptor ligand binding domain designated cancer, autolimune/inflammatory disorders, including allergy, inflammatory bowel disease, arthritis, psoriasis and respiratory tract inflammatory bowel disease, arthritis, psoriasis and respiratory tract inflammatory bowel disease, arthritis, psoriasis and respiratory tract inflammatory bowel or hypertension, oedema, angina, atherosclerosis, thrombosis, sepsis, shock, reperfusion injury, heart arrhythmia, and ischaemia, neurological disorders including central nervous system disease, Alzheimer's disease, brain injury, stroke, amyotrophic lateral sclerosis, anxiety, depression and pain, developmental disorders, metabolic disorders including diabetes mellitus, osteoporosis, lipid metabolism disorders, hyperthyroidism, hypercalcaemia, hypercholesterolaemia, hypercalcaemia, hypercholesterolaemia, glomerulonephritis, renovascular hypertension, dermatological disorders including acne, eczema and wound healing, negative effects of aging, acquired immunodeficiency syndrome (AlDS), viral, bacterial, fungal and acquired immunodeficiency syndrome (AlDS), viral, bacterial, fungal and sequence is a PCR primer used to isolate the coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                             New CAB55953.1 or LBDG3 polypeptide, useful as a nuclear hormone receptor ligand-binding domain, or for manufacturing of a medicament for diagnosing or treating cell proliferative disorders or
                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the protein and coding sequences of a
                                                                                                                                                                      Allen JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Major allergenic storage protein FAGAG1 PCR primer FAG19 SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.8%; Score 14.6; DB 6; Length 24; 61.9%; Pred. No. 4.8e+03; ive 4; Mismatches 4; Indels
                                                                                                                                                                      Pierron VN, Allen KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       food testing, allergen, PCR primer; Fagopyrum esculentum;
major allergenic storage protein; FAGAG1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 7 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                   Phillips T,
                                                                                                                                                                                                                                                                                                                                                                                         Example 2, Page 64; 122pp; English.
                                                                                                                                                                                                                                                                                                                                            autoimmune/inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 AGAGGGCUGGUUAAGGCGUC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AGAGGGCTTATTAACTCGTC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA24254 standard; DNA; 21 BP
                                          05-MAR-2002; 2002WO-GB000937
                                                                                     05-MAR-2001; 2001GB-00005402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Conservative
                                                                                                                           (INPH-) INPHARMATICA LTD
                                                                                                                                                                      Phelps CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fagopyrum esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                  WPI; 2002-698731/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003068964-A1
12-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-2003
                                                                                                                                                                                            Potter SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                        Fagan RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA24254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Gaps

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Length 21; 1; Indels Balog RP;

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This invention relates to a novel method for analysing chemically modified macromolecules. Specifically, it refers to a high throughput method for the parallel analysis of many potential sites of chemical modification (e.g. methylation) in DNA. The present invention describes treating the DNA with one or more chemical reagents that result in different base sequences depending upon the presence or absence of the modification of interest. Accordingly, a device comprising an array of probes is provided to hybridise with and select the altered DNA sequences that comprise the modifications of interest such as a CpG island. In particular, this invention refers to analysing the methylation pattern of a region of the promoter for the tumour suppressor gene pl6 from two human lung tumour cell lines H69 and H1618. This oligonucleotide sequence is a human DNA probe used to immobilise CpG methylated DNA of the
                                                                                                                                                                      Analysis of chemical modification of DNA involves obtaining sample of DNA to be analyzed, treating DNA with chemical reagents that result in different base sequences, and determining sequence of resulting DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Tespec PRO-3; testis specific serine protease; trypsin tamily serine protease; mature testis; sperm differentiation; sperm maturation; male infertility; sterility; reproductive disorder; sperm maturation; male infertility; sterility; reproductive disorder; contraception; rapid amplification of cDNA ends; RACE PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.2%; Score 14.2; DB 11; Length 21; 63.2%; Pred. No. 7.3e+03; ive 4; Mismatches 3; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 6 A; 11 C; 1 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Tespec PRO-3 5' RACE PCR primer, hPRO3-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                                                                                               Example 1; SEQ ID NO 474; 210pp; English
                                                                                                      Luebke KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 UGAGAGGGCUGGUUAAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 TGAGGGGTGCTGGTTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-JP006111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA61591 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 63.2
nes 12; Conservative
                                                                                                        Garner HR, Minna JD,
                                                                                                                                          WPI; 2003-874843/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-365604/31
                                  (MINN/) MINNA J D.
(LUEB/) LUEBKE K J.
(BALO/) BALOG R P.
                  GARNER H R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Senoo C, Numata M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200026352-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nvention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA61591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                (MINN/)
(LUEB/)
                  GARN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA6159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for modulating, in a host cell, a protein-protein interaction between a first protein which is PRAK (P38-CC regulated/activated protein kinsse or MPKARKS) and a second protein comprises administering to the cell a compound capable of modulating the comprises administering to the cell a compound capable of modulating the correction interaction. The method is useful in modulating in a host cell a protein interaction. The method is useful in modulating in a host cell a protein interaction between a first protein which is PRAX and a second protein which is ERA3 for treating inflammatory disorders, e.g., asthma, rheumatorid arthritis, juvenile chronic arthritis, myositis, crohn's disease, gastritis, colitis, ulcerative colitis, inflammatory bowel disease, proteitis, pelvic conjunctivitis, scleritis, chronic inflammatory polymeuropathy, Tertiary Lyme disease, psoriasis, dermatitis or eczema. In the exemplification of the present invention examples of antisense oligonucleotides specific to in SEQ ID NOS:11-223 (ADZ998069).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                               Modulating, in a host cell, a protein-protein interaction between first protein, PRAK, (MAPKAPKS) and second protein, ERK3, (extracellular signal-regulated kinase 3) by administering modulating compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probe; ss; chemical modification; methylation; array; CpG island;
tumour suppressor; p16; human; H69; H1618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human DNA probe used to immobilise CpG methylated DNA SegID 474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.2%; Score 14.2; DB 14; Length 20; 68.4%; Pred. No. 7.3e+03; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                Bush A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 4 A; 10 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                Mauck K,
                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 39; 296pp; English.
                                                                                                                                                                                                                Bartel P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGGCUGGUUAAGGCGUC 23
15-MAR-2001; 2001US-0276179P.
19-MAR-2001; 2001US-0277013P.
23-JUL-2001; 2001US-0301723P.
14-DEC-2001; 2001US-00014814.
21-DEC-2001; 2001US-00035343.
04-JAN-2002; 2002US-00035344.
14-MAR-2002; 2002US-00035344.
18-MAR-2002; 2002US-00035344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JUN-2002; 2002US-00184085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUN-2001; 2001US-0301370P
                                                                                                                                                                             MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ13347 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 68.4 les 13, Conservative
                                                                                                                                                                                                                Heichman K,
                                                                                                                                                                                                                                                  WPI; 2005-371623/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003152950-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2003
                                                                                                                                                                                                                Cimbora D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ß
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
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RESULT 15
ACD57816/c
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888888888888888888888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                      protesses (Respec PRO; AR801156_MBO1160) and to coDRAs encoding them (AAA61558-AG1562). It also encompasses expression vectors and host cells comprising a nucleotide sequence encoding a protesse of the invention, inhibitors of the protesses and antibodies against the protesses. The novel protesses are members of the trypsin family of serine protesses, having the serine and histidine active site signatures characteristic of this family. The protesses are specifically expressed in mature testis and participate in the differentiation and maturation of sperm. The protesses are potentially useful for the development of pharmaceuticals for the treatment of male infertility and other male reproductive disorders, and for the development of contraceptives. They may also be used as reagents for the diagnosis of male infertility. Sequences

AAA61550-A61553 represent RACE (rapid amplification of cDNA ends) PCR primers used in the isolation of cDNA encoding human Tespec PRO-3
                                                                                                                                                                                                                                                                                                                                                            ö
Trypsin family serine proteases expressed specifically in mature testis for development of methods for diagnosis and treatment of sterility and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                              The invention relates to novel murine and human testis specific serine
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss; probe; expressed sequence tag; microarray; gene expression;
tic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                               Score 14.2; DB 3; Length 25;
Pred. No. 7.4e+03;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human microarray DNA oligonucleotide SEQ ID NO 82768.
                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 4 A; 2 C; 10 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 82768; 9pp; English.
                                                    Example 9; Page 45; 121pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                     4 GAGGGCUGGUUAAGGCGU 22
                                                                                                                                                                                                                                                                                                                                                                                                    3 GATGGGCTAGTTAAGTCGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACI82777 standard; DNA; 25 BP
                                                                                                                                                                                                                                                                                                                                59.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-2002; 2002US-00098263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-2001; 2001US-0276759P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-567953/53.
                           for contraception.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003104410-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mittmann MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-2003
                                                                                                                                                                                                                                                                                (AAA61561)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACI82777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACI82777
 CCCXBXELETTXBXBXBXBXBXBXBXXBXXBXBXBXCCXCX
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CC haso disclosed is a method of gene expression analysis. The array is used in manitoring gene expression levels by hybridisation to a DNA library, an analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence in the method of analysis comprises in the probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the concleic acid further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-completic acid further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-comprises in mapping the 5' termini of mRNA molecules by primer extensions of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening segments of DNA that have been for additional subclones containing segments of DNA that have been concluded and previously sequenced. The sequence presented is one of the molecules acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amberzyme, G-cleaver ribozyme, decoy molecule, aptamer;
HBV reverse transcriptase; Enhancer I region, viral replication;
degenerative, disease state; HBV infection; HCV infection; cirrhosis;
liver failure; hepatocalular carcinoma; hepatotropic; cytostatic;
virucide; antiinflammatory; substrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 58.1%; Score 14; DB 9; Length 25; 1 Similarity 59.1%; Pred. No. 9.2e+03; 13; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25 BP; 6 A; 4 C; 10 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCV DNAzyme substrate sequence #514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GAGAGGGCUGGUUAAGGCGUC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACAGGGGATCGTTTAGACGTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACD57816 standard; RNA; 17 BP
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08-JUN-2001; 2001US-00877478.
08-JUN-2001; 2001US-026876P.
24-OCT-2001; 2001US-0335059P.
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05-DEC-2001; 2001US-0337055P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-2003 (first entry)
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MCSWIGGEN J.
MORRISSEY D.
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Best Local Similarity
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DRAPER K.
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(LEEP/)
(DRAP/)
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Blatt L, Macejak D,
Draper K, Roberts E;
                                                WPI; 2003-229207/22
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(ROBE/) ROBERTS E.

Mcswiggen J, Morrissey D, Pavco P, Lee P;

Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus infection. 

The present invention relates to nucleic acid molecules which modulate
the synthesis, expression and/or stability of Hepatitis C virus (HVV) or
Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
Inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
are nucleic acid decory molecules and aptamers that bind to HBV reverse
transcriptase and/or HBV reverse transcriptase primer sequences, as well
as oligonucleotides that specifically bind the Enhancer I region of HBV
DNA. The nucleic acids may be used to modulate the expression of HBV
compounds and/or potential therapise directed against HBV, and compounds
compounds and/or potential therapise directed against HBV, and compounds
that modulate the expression and/or replication of HCV. The compounds and
methods of the invention are useful for the treatment of degenerative and
disease states related to HBV and HCV infection, replication and gene
expression such as cirrhosis, liver failure, and hepatocellular
carcinoma. The present sequence represents a substrate for one of the HCV
DNAzyme or minus strand DNAzyme sequences disclosed in the present Claim 1; Page 243; 387pp; English.

Sequence 17 BP; 4 A; 9 C; 1 G; 0 T; 3 U; 0 Other;

Gaps ö Query Match

S7.5%; Score 13.8; DB 8; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.1e+04;
Matches 12; Conservative 3; Mismatches 2; Indels

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6 GGGCUGGUUAAGGCGU 22

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17 GGGCAGGTTAAGGTGT 1

Search completed: October 16, 2006, 14:15:57 Job time : 128.594 secs

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PAT 03-JUL-2002
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CS102090 Sequence
ARC40243 Sequence
ARI50048 Sequence
ARI50048 Sequence
ARI50043 Sequence
AR27916 ARI580EC
AR213127 Sequence
AR213127 Sequence
CS02086 Sequence
AR404657 Sequence
AR404657 Sequence
AR404657 Sequence
AR534679 Sequence
AR13984 Sequence
AR13984 Sequence
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Best Local Similarity 73.7%; Pred. No. 6.2e+04;
Matches 14; Conservative 3; Mismatches 2;
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/organism="synthetic construct"
/mol_typo="unassigned DNA"
/db_xref="taxon:32630"
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Probes and decoder oligonucleotides
Parent: WO 0216649-A 365 28-FEB-2002;
Illumina, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other sequences; artificial sequences
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AR231257
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AX004269
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GAGAGGCGTTGGTTAAGGC 22
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AX447886
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AX538707 Sequence
AX538707 Sequence
129861 Sequence
129861 Sequence
129861 Sequence
129861 Sequence
12020 Sequence
AX215297 Sequence
AX215299 Sequence
AX215299 Sequence
AX215299 Sequence
AX215299 Sequence
AX215390 Sequence
                                                                                                              ; Search time 590.797 Seconds (without alignments) 2597.742 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                   GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                           1796954
                                                                                                                                                                                                                                                                                          6366136 seqs, 31973710525 residues
                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                  nucleic search, using sw model
                                                                                                                 October 16, 2006, 13:57:30
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AX447866
AX63786470
AR036420
129861
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BD1417868
BD1817368
BD181736
AX15297
AX215297
AX215299
AX215299
AX215308
AX215308
AX347840
AX347840
AX347840
AX369552
CS101953
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Gapop 10.0 , Gapext 1.0
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24
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Match
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Perfect score:
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PAT 06-FEB-1997
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Novel G protein coupled receptor protein and its DNA FH
Location/Qualifiers
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Location/Qualifiers
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                                         Length
                                                                                                                                                                                                                                                                                          Unclassified.

1 (bases 1 to 22)
Seizinger,B.R., Kley,N.A. and Bianchi,A.B.
WF2 isoforms
Patent: US 5578462-A 12 26-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

57.5%; Score 13.8; DB 2;
Best Local Similarity 70.6%; Pred. No. 5.4e+05;
Matches 12; Conservative 3; Mismatches 2;
                                    Score 13.8; DB 2;
Pred. No. 5.4e+05;
3; Mismatches 2;

    .28
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                                                                                                                                                                                           22 bp | Sequence 12 from patent US 5578462. 129861
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/organism="unknown"
/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
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                                                                                             17 AGAGGAGCTGGTTCAGG 1
                                      Query Match 57.5%;
Best Local Similarity 70.6%;
Matches 12; Conservative
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BD141786
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129861/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fagan, R.J., Phelps, C.B., Phillips, T., Pierron, V.N., Allen, K.E., Allen, J.M. and Potter, S.J.
Nuclear hormone receptor ligand binding domain
Patent: WO 2070557-5 6 12-SEP-2002;
Inpharmatica Limited (GB)
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                                                                                             1. .25
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                                                                                                                                                                                             Query Match 65.8%; Score 15.8; DB 2; Length 25; Best Local Similarity 73.7%; Pred. No. 6.1e+04; Matches 14; Conservative 3; Mismatches 2; Indels
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Seizinger, B.R., Kley, N.A. and Bianchi, A.B.
NF2 isoforms
Patent: US 5872214-A 12 16-FEB-1999,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .24
/organism="synthetic construct"
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/db_xref="teaxon:32630"
/noTe="LBDG3 Reverse primer"
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                                       Probes and decoder oligonucleotides
Patent: WO 0216649-A 4341 28-FEB-2002;
Illumina, Inc. (US)
Location/Qualifiers
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 other sequences; artificial sequences
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Sequence 12 from patent US 5872214.
AR036420
AR036420.1 GI:5953088
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Sequence 6 from Patent WO02070557.
AX538707
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synthetic construct
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Best Local Similarity
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                          Gunderson, K.
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AR036420/c
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AX538707/c
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AUTHORS
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KEYWORDS
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SOURCE ORGANISM

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DEFINITION ACCESSION VERSION KEYWORDS

BD173668 LOCUS

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Matches

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PC A61P25/08,
PC A61P25/08,
PC A61P25/08,
PC CO7K16/28,A61P27/16,A61P29/00,A61P31/04,A61P37/08,A61P43/00,
PC CO7K16/28,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/
PC CO7K16/28,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/
PC G01N33/50,G01N33/50,G01N33/53,G01N33/566//A61K31/7125 PC
A61K31/713,A61K35/76,
PC A61K48/00,C12N15/00,C12N5/00
CC NOVel G procein coupled receptor protein and its DNA FH Key
Location/Qualifiers
OS Artificial Sequence
PN 072335977-A/34
PD 26-NOV-2002
PP 23-AUG-2001 JP 2001252855
PI YASUKO TERAO, YASUSHI SHINTANI
PC C12N15/09, A61R45/00, A61P1/04, A61P1/10, A61P1/12, A61P1/14, A61P1/
PC 16, A61P1/18,
PC 16, A61P9/10, A61P9/10, A61P9/12, A61P11/00, A61P11/06, A61P13/ PC
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Smith, K.E., Borden, L.A., Weinshank, R.L. and Hartig, P.R.
DNA encoding taurine and GABA transporters and uses thereof
Patent: US 6225115-A 23 01-MAY-2001;
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Pred. No. 1e+06;

    .28
    ^organism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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Sequence 23 from patent US 6225115.
AR148541

    .25
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    /mol_type="unassigned DNA"

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Sequence 23 from patent US 5658786.
162320
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AR148541/c
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162320/c
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C12P21/08
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PF 02-FEB-2001 JP 01P 026798
PI TETSUYA OTAKI YASUSHI MASUDA, YOSHIHIRO TAKATSU PC
C12N15/12,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C07K14/ PC
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                                                                                                                                                                                                                                                                                                                                                      synthetic construct
synthetic construct
other sequences; artificial sequences.
(Dases I to 28)
Otaki,T., Masuda,Y. and Takatsu,Y.
Novel physiologically active peptide and use thereof
Patent: WO 02062996-A 23 15-AUG-2002,
TAKEDA CHEMICAL INDUSTRIES LTD,TETSUYA OTAKI,YASUSHI MASUDA,
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BD181737
BD181737.1 GI:30792655
JP 2002335977-A/34.
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Novel physiologically active peptide and use thereof.
BD173668
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synthetic construct
other sequences artificial sequences.
( bases 1 to 28)
Terao, Y. and Shintani, Y.
Novel G protein coupled receptor protein and its DNA
Patent: JP 2002335977-A 34 26-NOV-2002;
TAKEDA CHEMICAL INDUSTRIES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ice 1..28
/organism='Artificial Sequence'
Location/Qualifiers
                                                      ch 55.8*; Score 13.4; DB 2; Length 28;
l Similarity 60.9*; Pred. No. 7.9e+05;
14; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.8%; Score 13.4; DB 2; Length 28; 60.9%; Pred. No. 7.9e+05;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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   /db_xref="taxon:32630"
                                                                                                                               1 UGAGAGGGCUGGUUAAGGCGUC 23
                                                                                                                                                     1 UGAGAGGGCUGGUUAAGGCGUC 23
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WO 02062996-A/23
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WO 02062996-A/23.
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REFERENCE AUTHORS TITLE JOURNAL

Matches

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PAT 07-SEP-2001
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 741 16-AUG-2001;
RIBOXYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 742 16-AUG-2001;
RIBOZYME PHARMACEUTIALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) McSwiggen, James (US) ; Chowrira, Bharat M. (US) Location/Qualifiers
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Pred. No. 1.4e+06;
2; Mismatches 0;
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                                                    1..17
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/mol_type="unassigned RNA"
/nol_e="Nucleic Acid"
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synthetic construct
other sequences; artificial sequences.
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Sequence 742 from Patent WO0159103.
AX215300
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synthetic construct
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les 11; Conservative
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15 TGAGGGGCTGG 3
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AX215300/c
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AX215299/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blatt, L., Mcswiggen, J. and Chowrira, B.M. Method and reagent for the modulation and diagnosis of cd20 and motor game expression patent: WO 0159103-A 739 16-AUG-2001; Patent: WO 0159103-A 739 16-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US); McSwiggen, James (US); Chowrira, Bharat M. (US)
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Smith, K.E., Weinshank, R.L., Borden, L.A. and Hartig, P.R.
DNA encoding rat taurine transporter and uses thereof
Patent: US 568786-A 23 19-AUG-1997;
Location/Qualifiers
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Patent: WO 0159103-A 740 16-AUG-2001;
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AX215298
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Sequence 739 from Patent WO0159103.
AX215297
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Best Local Similarity 66.7%;
Matches 12; Conservative
        GI:2480268
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Matches 11; Conservative
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Bachmanov, A.A., Beauchamp, G.K., Chatterjee, A., de Jong, P.J., Li, S., Li, X., Ohmen, J.U., Reed, D.R., Ross, D. and Tordoff, M.G. Gene and sequence variation associated with sensing carbohydrate compounds and other sweeteners
Patent: WO 0183749-A 407 08-NOV-2001;
WARNER-LAMBERT COMPANY (US); The Monell Chemical Senses Center (US)
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Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
                                                                                                                                     Gaps
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1. 20
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Sequence 407 from Patent WO0183749.
AX298773.1 GI:17128763
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Query Match

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Search completed: October 16, 2006, 14:52:12 Job time : 591.797 secs

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Run on:

Sequence:

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Balzergue, S.

Balzergue, S.

Direct Submission

Submitted (12-0CT-2003) Balzergue S., UWRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR ware directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
program 'Genoplante' (http://www.genoplante.com and
'http://genoplante-info.infologen.fr).

Location/Qualifiers
                               A2945526 ZM0206122
A2948983 ZM0212C15
A2948983 ZM0212C15
A2441037 1M0202023
A2602448 ZM0051B20223
A26743020 1BB6E06.F
A2976285 ZM0251H09
A118338 Gd41a12.x
AL498874 T. brucei
A2346729 1M0082A10
A2851549 ZM0153P13
A2851549 ZM0153P13
A27854549 ZM0153P13
A278256 01119113D0
A2591936 1M0402J20
C2777040 1119946G1
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A27825016 1M0407C19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chavvin, S., Bechlold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T_DNA integration into the Arabidopsis genome depends on sequences
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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EMBO Rep. 3 (12), 1152-1157 (2002)
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AZ346729
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 AJS91134 Arabidops
AZ806300 ZM0068F13
CZ443094 IBBBD03.f
AG473941 tm04c11.x
R89803 yp91b12.r1
AG613296 Escherich
AJS31105 Arabidops
AZ346559 1M0081M15
AZ654730 1M0529P05
AZ970595 ZM0243118
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AZ820085 ZM0092001
AJS91135 Arabidops
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AJS91135 Arabidops
AZ846437 ZM0146E10
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                 GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                          AZ806300 24 bp DNA linear GSS 20-FEB-2001 2M0068F13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0068F13 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Unpublished (2000)
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XLI0-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42tv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                       /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dun, Da. 9. 12. 2. 1. Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                            ô
                                                                                                                                                                              Score 13.4; DB 14; Length 27; Pred. No. 3.1e+05;
                                                                                                                                                                                                                          1; Indels
                                /ecotype="Wassilewskija"
1. 27
/note="T-DNA flanking sequence
left border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0068 row: F column: 13
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:10090"
/clone="UUGC2M0068F13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
/clone="580B05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ806300.1 GI:12967111
GSS.
                                                                                                                                                                           55.8%;
                                                                                                                                                                                                                                                                      5 AGGGGCUGGUUAAGG 19
                                                                                                                                                                                                                                                                                               21 AGGGCTGGTTAACG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 24)
                                                                                                                                                                                                                          11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .24
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308, b.
USA
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                                                                     misc_feature
                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
AZ806300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
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                                                                                                                                      DRIGIN
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/coll line="Jurkar"
/clone_lib="HIV-vector integration sites from
well-expressed provinces in human Jurkat T cells"
/clone_lib="HIV-vector integration sites from
well-expressed provinces in human Jurkat T cells"
/note="Vector: LTR-Tat-IRES-GFP (PEV731); We have
investigated regulatory sequences in noncoding human bhat care associated with repression of an integrated human
immunodeficiency virus type 1 (HIV-1) promoter. HIV-1
integration results in the formation of precise and
homogeneous junctions between viral and host DNA, but
integration takes place at many locations. Thus, the
variation in HIV-1 gene expression at different
integration attes reports the activity of regulatory
sequences at nearby chromosomal positions. Negative
regulation of HIV transcription is of particular interest
because of its association with maintaining HIV in a
latent state in cells from infected patients. To identify
chromosomal regulators of HIV transcription, we infected
Jurkat T cells with an HIV-based vector transducing green
fluorescent protein (GFP) and separated cells into
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 07-APR-2005
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1 (Dases 1 to 28)
Lewinski, M.K., Bisgrove, D., Shinn, P., Chen, H., Hoffmann, C., Hannenhalli, S., Verdin, E., Berry, C.C., Ecker, J.R., and Bushman, F.D. Genome-wide analysis of chromosomal features repressing human immunodeficiency virus transcribtion

J. Virol. 79 (11), 6610-6619 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CZ443094
IBB8D03.fwd HIV-vector integration sites from well-expressed proviruses in human Jurkat T cells Homo sapiens genomic clone IBBBD03.fwd, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Microbiology
University of Pennsylvania School of Medicine
402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA
19104-6076, USA
Tel: 215 573 8732
Fax: 215 573 4856
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                52.5%; Score 12.6; DB 11; Length 24; llarity 57.9%; Pred. No. 6.9e+05; Conservative 4; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bushmandmail.med.upenn.edu
Class: PCR with specific primers.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="IBBBD03.fwd"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 UGAGAGGGCUGGUUAAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s receaerecerectrace 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Bushman FD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Virol.
15890899
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25 bp mRNA linear EST 24-AUG-1995
yP91b12.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
IMAGE:194783 5' similar to gb:X63526 ELONGATION FACTOR 1-GAMMA
(HUMN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-Werck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1193
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; race considered overall poor quality
Insert Length: 1193 Std Error: 0.00
Seq primer: MI3RPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae, Homo.

1 (bases 1 to 25)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hellman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3763833"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/clone="IMAGE:194783"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                        20 cacaceceacerceacece 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   R89803.1 GI:954630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson, R.
                                             N
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                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
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JOURNAL
COMMENT
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                                                                                                                                                                                                             RESULT 5
R89803/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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populations containing well-expressed (GFP-positive) or poorly expressed (GFP-negative) proviruses. We then determined the chromosomal locations of the two classes by sequencing 971 junctions between viral and cellular DNA. Possible effects of endogenous cellular transcription were characterized by transcriptional profilling, Low-level GFP expression correlated with integration in (i) generates, (ii) centromeric heterochromatin, and (iii) very highly expressed cellular genes. These data provide a genome-wide picture of chromosomal features that repress transcription and suggest models for transcriptional latency in cells from HIV-infected patients."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A1473941 22 bp mRNA linear EST 09-MAR-1999 tm04c11.x1 NCI CGAP Co14 Homo sapiens cDNA clone IMAGE:2155604 3' similar to TR:\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\overline{0}\)0645\(\
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/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae, Homo.

1 (bases 1 to 22)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 50.8%; Score 12.2; DB 13; Length 28; Best Local Similarity 64.7%; Pred. No. 1.1e+06; Matches 11; Conservative 3; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Score 12; DB 1; Length 22; 70.0%; Pred. No. 1.3e+06;
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Seg primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AGAGGGCCUGGUUAAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI473941.1 GI:4326986
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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ORGANISM
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AUTHORS
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KEYWORDS
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Gaps

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Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
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1 (bases 1 to 29)
5 Dunn,D., Aoyagai,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Rilam,H., Longacze,S., Mahmoud,M., Menen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

1 (1000) Muse whole genome scaffolding with paired end reads from 10kb plasmid inserts
1 (1000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ346559 1908 10kb plasmid UUGCIM library Mus musculus genomic UUGCIM0081M15 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3702"
/clone="225H06"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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                                                                                                                                                                                                                                                                                                                       1. .28
Organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/cultivar="Wassillewskija"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="T-DNA flanking sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Tel: 801 585 7177
Tel: 801 685 7177
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Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /ecotype="Wassilewskija"
1. .28
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Location/Qualifiers
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AZ346559.1 GI:10425796
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Best Local Similarity
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AZ346559
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KEYWORDS
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                                                                                                            GSS 24-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (19-JAN-2004) Takashi Horiuchi, National Institute for Basic Biology, Gene Expression and Regulation II; 38 Nishigo-naka, Myodaijicho, Okazaki, Aichi 444-8585, Japan (E-mail:kishori@nibb.sc.jp, Tel:81-564-55-7690, Fax:81-564-55-7695) Location/Qualifiers
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AJ531105.1
GI:26799365
GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Ahalvin, S., Bechtold, N., Craud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                 Hayashi,K., Morooka,N., Mori,H. and Horiuchi,T.
A more accurate sequence comparison between genomes of Escherichia
coli K12 W3110 and MG1655 strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="The 5' end of this sequence corresponds to 9729(c)
                                                                                                                                                                                                                                                  Bscherichia coli K12
Escherichia coli K12
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
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                                                                                                     AG613296 27 bp DNA linear GSS 24-J.
Escherichia coli K12 MG1655 DNA, clone: 431F, genomic survey
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This is located within REP element."
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/mol_type="genomic DNA"
/strain="K12"
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Hayashi, K., Morooka, N. and Horiuchi, T.
Direct Submission
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                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae; Escherichia.
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/db_xref="taxon:8333"
/clone="431F"
                                                                                                                                                                                                   GI:41224745
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Balzergue, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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AG613296.1
                                                                                                                                                           sequence.
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SOURCE
ORGANISM
                                                           RESULT 6
AG613296/c
                                                                                                          LOCUS
DEFINITION
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AUTHORS
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REFERENCE
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PUBMED
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                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pw042 (gi|4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xili0-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah Genome Center
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Weiss B. Second B. S
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 21)
                                                                                                                            /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: FWP4Zrv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Brror: 0.00
Plate: 0529 row: P column: 05
Seg primer: CGTTGTAAAACGACGGCCAGT
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/db_xref="taxon:10090"
/clone="UUGC1M0081M15"
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Location/Qualifiers
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                                                                                            /sex="Male
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Fax: 801 585 7177
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/ General Continuo 25703
/ Faboute 1000-1000 Strain XL10-Gold, Tl-resistant, F-"
/ Calone 11br Mouse 1000 Plasmid UGCIM library.
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/ Alone 11br Mouse 1000 Plasmid UGCIM library.
/ Alone 11br Mouse DNA Resource
/ Alone 11br Mouse DNA Resource
(http://www.jax.org/resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMNAC (gil 4772114 [gb] AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA. and transformed into
chemically-competent E. coli XL10-Gold (stratagene) cells
and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.

1 (bases 1 to 27)
Bun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niedrhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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2M0243I18R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0243I18 R, genomic survey sequence.
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Insert Length: 10000 Std Error: 0.00
Plate: 0243 row: I column: 18
Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
mol_type="genomic DNA"
'strain="C57BL/6J"
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                                                           /db_xref="taxon:10090"
/clone="UUGC1M0529P05"
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Fax: 801 585 7177
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3; Mismatches
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/organism="Zea mays"
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Best Local Similarity 61.1%;
Matches 11; Conservative
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CG725093.1 GI:37
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AUTHORS
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COMMENT
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                                                                                                       /lab_hogt="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone library"
/note="Vetor: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
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1 (bases 1 to 27)
Walbot, V.
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Stanford University
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Reverse complemented post-ligation sequence from source sequence.

Plate: 1119029 row: H column: 12
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/culfivar=mixed background W23/A188/B73/K55"
/db xref="taxon:4577"
/ti§sue_type="leaf"
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48.3%; Score 11.6; DB 11; Length 27;
Best Local Similarity 61.1%; Pred. No. 1.9e+06;
Matches 11; Conservative 3; Mismatches 4; Indels (
                                                                                                                                                                                                 Laboratory Mouse DNA Resource
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                         _xref="taxon:10090"
                                                                /clone="UUGC2M0243I18"
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1 GGGAGTGGGTGGTTAGGG 18
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/dev stage="adult"
/lab_host="BH10B"
/clone lib="lill9 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site i: BamHi; Site 2: BgJII;
RescueMu is a 4.9 kb, modiffed maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units; For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BgIII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
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1119083H11.2EL_Y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
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Unpublished (2001)
Contact: Walbot V
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855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 8221

Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119083 row: H column: 11
Class: transposon-tagged.
Location/Qualifiers
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinae. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwadz (gil #712114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0048 row: M column: 20
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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Mus musculus
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AZ375590.1 GI:10489290
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                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
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84112, USA
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AZ375590/c
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Drosophila melanogaster DNA, clone:1(2)SH2 0127, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-MR-2002) Suwan Oh, The Laboratory of Immunobiology, National Institutes of Health, National Cancer Institute, Frederick, 1050 Boyles st., Frederick, Maryland 21702-1201, USA (E-mail:ohsuwan@mail.ncifcrf.gov, Tel:1-301-846-7314, Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
1 (bases 1 to 25)
       BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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A p-element inscrtion screen identified mutations in 455 novel essential genes in Drosophila Genetics 163 (1), 195-201 (2003)
                                                                                                                                                                                        Gaps
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oh,S., Kingsley,T., Shin,H., Zheng,Z., Chen,H. and Hou,S. Direct Submission
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/mol type="genomic DNA"
/db xref="taxon:7227"
/clone="1(2)5H2 0127"
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Gaps

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GSS 02-OCT-2000

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REPRENCE
In (Dases 1 to 30)
AUTHORS
DIAM D. AOyagl.A., Barber.M., Bascorn.T., Duval.B., Hamil.C.,
Rilam.D., Aoyagl.A., Barber.M., Mescon.E., Pedersen.T.,
Rilam.D., Aoyagl.A., Rose, M., Mescon.E., Pedersen.T.,
Rilam.D., And Wright.D., Walss.M., Tingey, A., von
TITLE
Notes whole genome scaffolding with paired end reads from 10kb
Jannia Inserter
Contest: Robert.B. Weiss
University of Urah Genome Center
Rm. 308 Moundaired Non
Rm. 308 Moundaired Secon
Fax: 801 385 506
Fax: 802 Fax:
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Query Match 47.5%; Score 11.4; DB 11; Length 30; Best Local Similarity 52.4%; Pred. No. 2.4e+06; Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps

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Search completed: October 16, 2006, 15:51:23 Job time : 1034.18 secs

41852, A 58488, A 73489, A 78586, A 122139,

Sequence Sequence Sequence

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102, App 65, Appl 65, Appl 11, Appl

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

9132, Ap 440, App 6, Appli

Sequence

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Perfect score:

Sequence:

nucleic

Run on:

Scoring table:

Searched:

Database

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ADDRESSEE: No. 6015783disk of No. 6015783th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,052
FILING DATE: 06-MAR-1997
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Blias J
REGISTRATION NUMBER: 33,728
REGISTRATION NUMBER: 4684.204-US
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 53, Application US/08814052
Patent No. 6015783
GENERAL INFORMATION:
APPLICANT: von der Osten, Claus
APPLICANT: Cherry, Joel R.
APPLICANT: Application Michael Dolberg
APPLICANT: Nind, Jeesper
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
TITLE OF INVENTION: OR STAINS FROM CELLULOSIC FABRIC
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6015783 to No. 6015783 th America,
STREET: 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                 US-09-630-377-11
US-09-396-196G-41852
US-09-396-196G-73489
US-09-396-196G-73489
US-09-396-196G-72139
US-09-396-196G-122130
US-09-396-196G-122140
US-09-422-978-9132
US-09-422-978-9132
US-08-117-952-440
US-09-526-193A-6
                   US-09-402-776-65
US-09-402-776-102
US-09-291-129-10
US-08-470-246-65
US-08-316-75-65
US-08-316-765-65
US-09-724-475-102
US-09-724-475-102
US-09-724-475-102
US-09-724-475-102
US-09-724-475-102
US-09-724-475-102
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SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Sequence 23, Appl
Sequence 23, Appl
Sequence 7, Appl
Sequence 31, Appl
Sequence 113, Appl
Sequence 119, Appl
Sequence 119, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 51, Appl
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                                                                                                                                                                                     October 16, 2006, 14:11:03; Search time 55.5789 Seconds (without alignments) 807.979 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued Patents_Nh:*

| / EMC Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
| / EMC Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
| / EMC Celerra_SIDS3/ptodata/2/ina/6_COMB.seq:*
| / EMC Celerra_SIDS3/ptodata/2/ina/6_COMB.seq:*
| / EMC Celerra_SIDS3/ptodata/2/ina/f_COMB.seq:*
| / EMC Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
| / EMC Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
| / EMC Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
| / EMC Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                            GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1097684
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S-09-443-067-45
S-09-396-196G-3644
S-09-396-196G-29254
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-09-396-196G-15707
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US-09-396-1570-18-12

US-08-628-145-12

US-08-295-814E-23

US-09-343-316-23

US-09-46-18-23

US-09-641-259B-31

US-09-641-259B-31

US-09-641-259B-31

US-09-641-259B-31

US-09-659-579A-123

US-09-396-166-16

US-09-396-166-364

US-09-396-196G-3644

US-09-396-196G-365

US-08-840-316-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1403666 segs, 935554401 residues
                                                                                                                                                                                                                                                                                                                                                         1 ugagagggcugguuaaggcgucc 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                        US-10-604-726A-6034
24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                     Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 30
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Match
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Length 28;

DB 3;

63.3%; Score 15.2;

US-08-814-052-53

Query Match

Sequence Sequence (

Sequence

13.28

8 Result

125.66 12

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                                                                                                                                                                                                                                                                                                            57.5%; Score 13.8; DB 2; Length 22; 70.6%; Pred. No. 2.5e+03; Live 3; Mismatches 2; Indels
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Pred. No. 2.5e+03;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,145
FILING APPLICATION 1930
FILING RAPLICATION NUMBER: US 08/179,738
FILING DATE: 10-JAN-1994
ATTOMENYAGENT INFORMATION:
ANAMERIA DELOCATION:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-628-145-12/C

Sequence 12, Application US/08628145

Sequence 12, Application US/08628145

Patent No. 5872214

GENERAL INFORMATION:
APPLICANT: Seizinger, Bernd R.
APPLICANT: Riey, Nikolai A.
APPLICANT: Bianchi, Albert B.
TITLE OF INVENTION: No. 5872214el NF2 Isoforms

VUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robins
STREET: 615 Bryant Street

CITY: Palo Alto
STATE: California

COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Robins, Roberta L.
REGISTRATION UNDBER: 33.208
REFERENCE/DOCKET NUMBER: 5998-0017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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Best Local Similarity 70.6%;
Matches 12; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 22 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                       12; Conservative
                                                                                                                                                  single
                                                                                                                                       STRANDEDNESS: Bing
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Matches 12; Conserva
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                                              Indels
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ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: DATE:

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/179,738

FILING DATE: 10-JAN-1994

CLASSIFICATION: 530

ATORNEY/AGENT INFORMATION:

NAME: RObins, Roberta L.

REGISTRATION NUMBER: 33,208

REGISTRATION NUMBER: 33,208

REGISTRATION NUMBER: 33,208

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRAX: (415) 617-8999
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Sequence 12, Application US/08179738
Sequence 12, Application US/08179738
Sequence 12, Application US/08179738
Sequence 12, Application Setzing Nikolai A. APPLICANT: Bianchi, Albert B. TITLE OF INVENTION: No. 5578462el NF2 Isoforms INVENES OF SEQUENCES: ADDRESSE: Reed & Robins STREET: 635 BYPANT Street CITY: Palo Alto STREE: California
STREET: California
STREET: California
          Pred. No. 5.5e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                        Sequence 15707, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REPRENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 80/100,678
SPROR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SSGFWARRE: PRESEEQ for Windows Version 4.0
SEQ ID NO 15707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 TGAGATGAGCTGCTTAACGAGT 1
                                                                                                                  2 GAGAGGGCUGGUUAAGGCG 21
                                                                                                                                                         20 GCGAGTGGCTGGTCAAGGCG 1
          75.0%;
          Best Local Similarity 75.0 Matches 15; Conservative
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-15707
                                                                                                                                                                                                                                                                                      RESULT 2
US-09-396-196G-15707/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-179-738-12/c
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Squence 7, Application US/0959892C

Squence 7, Application US/0959892C

Squence 10. 698260

GENERAL INFORMATION:

APPLICANT: Niles, Andrew

APPLICANT: Haak-Frendscho, Mary

APPLICANT: Haak-Frendscho, Mary

APPLICANT: Haak-Frendscho, Mary

ITLE OF INVENTION: RECOMBINANT PROTECLYTIC TRYPTASES, ACTIVE SITE MUTANTS THEREOF,

ITLE OF INVENTION: AND METHODS OF MAKING SAME

FILE REFERENCE: 3456.104

CURRENT APPLICATION NUMBER: US/09/598,982C

CURRENT FILING DATE: 1998-04-15

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin version 3.3

SEQ ID NO 7

LENGTH: 27
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Scheders, Stephen
APPLICANT: Schneider, Michael
TITLE OF INVENTION: DISEASE GENE, DIAGNOSTICS AND TREATMENT
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
COUNTRY: U.S.A.
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      Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.2%; Score 13; DB 4; Length 27; 66.7%; Pred. No. 6.2e+03; 1ive 2; Mismatches 5; Indels
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
    Score 13.2; DB 3;
Pred. No. 4.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Mutagenesis oligonucleotide
US-09-598-982C-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/413,580
FILING DATE: 03-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/460,751
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GAGGGCUGGUUAAGGCGUCC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/08460751
Patent No. 5891628
GENERAL INFORMATION:
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GAGGAGCCGGTGAAGGTCTCC 21
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                       5 AGGGCUGGUUAAGGCGU 22
                                                                                                                              23 AGGTGCTGGTGAAGGCAT 6
S5.0%;
Local Similarity 66.7%;
les 12; Conservative 3
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Matches 14; Conservative
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US-08-460-751-27
        Query Match
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                       Best Loca
Matches
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Patent No. 622515
GENERAL INFORMATION:
APPLICATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DNA Encoding Taurine and GABA Transporters and Uses
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
CURRENT APPLICATE: 1999-06-30
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0 - beta
SEQ ID NO 23
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
               Sequence 23, Application US/08295814E
Patent No. 5658786
GENERAL INFORMATION:
APPLICANT: Smith, Kelli E.
APPLICANT: Borden, Laurence A.
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING TAURINE AND GABA; TITLE OF INVENTION: TRANSPORTERS AND USES THEREOF NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.2; DB 2;
Pred. No. 4.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAPELICATION DATA:
APPLICATION NUMBER: US/08/295,814E
FILING DATE: DECEMBER 19, 1994
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAWE: White, John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40558-B-PCT-TELECOMMUNICATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                    B: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 25 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AGGGCUGGUUAAGGCGU 22
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Best Local Similarity 66.7%
                                                                                                                                                                                                                                                                          STREET: 1185 Aver CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-295-814E-23
    US-08-295-814E-23/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-343-361-23/c
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APPLICANT: FACKLER, MACUAL APPLICANT: FACKLER, MACUAL APPLICANT: FACKLER, MACUAL APPLICANT: FACKLER, MACUAL APPLICANT: APPLICANTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY FILE REFERENCE: JUL1630-1
CURRENT APPLICATION NUMBER: US/10/059,579A
CURRENT PILING DATE: 2001-01-28
PRIOR APPLICATION NUMBER: US 09/771,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pacquence 199, Application US/09166186A

Pacquence 199, Application US/09166186A

Pacquence 119, Application US/09166186A

Pacquence 110, Application US/09166186A

APPLICANT: Bareria

APPLICANT: Butler, Madeline M.

APPLICANT: Branchan, William R.

TITLE OF INVENTION: 1SPH-0322

CURRENT APPLICATION NUMBER: US/09/166,186A

CURRENT APPLICATION NUMBER: US/09/166,186A

NUMBER OF SEQ ID NOS: 250

SEQ ID NO 119

LENGTH: 20
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APPLICANT: Baker, Brenda
APPLICANT: Bannet, C. Frank
APPLICANT: Butler, Madeline M.
APPLICANT: Shanahan, William R.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: ISPH-0356
CURRENT APPLICATION UNIBER: US/09/313,932A
CURRENT FILING DATE: 1999-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.5%; Score 12.6; DB 3; Length 19; Best Local Similarity 57.9%; Pred. No. 9.1e+03; Matches 11; Conservative 4; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: PCR antisense primer US-10-059-579A-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: antisense sequence US-09-166-186-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 119, Application US/09313932A
Patent No. 6228642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GAGGGCUGGUUAAGGCGU 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GAGGGCUGGUUAAGGCGU 22
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ORGANISM: Artificial Sequence
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Matches 12; Conservative
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US-09-313-932-119/c
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US-09-166-186-119/c
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US-10-059-579A-123/c
is sequence 123, Application US/10059579A
is patent No. 6835541
is GENERAL INFORMATION:
is APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
is APPLICANT: SUKMANA, Saraswati
is APPLICANT: EVRON, Ella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31, Application US/09641259B

patent No. 6468756

GENERAL INFORMATION:
APPLICANT: Bonini, James A
APPLICANT: Bonowsky, Beth E
APPLICANT: Borowsky, Beth E
APPLICANT: Adham, Nika
APPLICANT: Thompson, Thelma O.
TITLE OF INVENTION: DNA Encoding SNORF25 Receptor
FILE REPRENCE: 1795/56095-B/JPW/ADM
CURRENT APPLICATION NUMBER: US/09/641,259B
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US/09/4413
PRIOR PILING DATE: 1299-08-13
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 35
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3.1
ATTORNEY/AGENT INFORMAL.

NAME: COLUZZI, LAURA A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7638-005

TELECOMMUNICATION INFORMATION:
TELEFPHONE: (212) 869-8864/9741

TELEFAX: (212) 869-8864/9741

TELEFAX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs

LENGTH: 19 base pairs

LENGTH: 19 base pairs

TELEFAX: 1019 base pairs

TELEFAX: 66141 ENNIE

TELEFAX: 66141 ENNIE

TELEFAX: 66141 ENIE
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-460-751-27
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US-09-641-259B-31/c
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GENERAL INFORMATION:
APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
APPLICANT: ORGANISATION
TITLE OF INVENTION: Polyphenol oxidase genes from banana, lettuce, tobacco and
TITLE OF INVENTION: pineapple
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12.6; DB 3;
Pred. No. 9.2e+03;
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Pred. No. 9.5e+03;
               CURRENT APPLICATION NUMBER: US/08/520,373D
CURRENT FILING DATE: 1995-08-29
PRIOR APPLICATION NUMBER: 08/377,710
PRIOR APPLICATION NUMBER: 08/377,710
PRIOR APPLICATION NUMBER: 08/279,979
PRIOR FILING DATE: 1994-07-25
PRIOR FILING DATE: 1992-06-04
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR APPLICATION NUMBER: 07/952,796
PRIOR FILING DATE: 1992-06-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE KEFEKENCE:
CURRENT PELLICATION NUMBER: US/09/443,067
CURRENT FILING DATE: 1999-11-18
EARLIER APPLICATION NUMBER: US 08/976, 222
EARLIER PILING DATE: 1997-11-21
EARLIER PPLICATION NUMBER: PCT/AU98/00362
EARLIER PILING DATE: 1998-05-19
EARLIER PILING DATE: 1998-05-23
EARLIER PILING DATE: 1998-05-23
EARLIER FILING DATE: 1997-05-19
EARLIER FILING DATE: 1997-09-26
NUMBER: OF SEQ ID NOS: 49
SOFTWARE: PALENT ON NUMBER: AU PP5600
EARLIER FILING DATE: 1995-09-26
NUMBER: OF SEQ ID NOS: 49
SOFTWARE: PALENT ON VOWER: AU PP5600
EARLIER FILING DATE: 1995-09-26
NUMBER: OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.5%; Score 12.6; D
Best Local Similarity 63.2%; Pred. No. 9.2e
Matches 12; Conservative 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45, Application US/09443067 Patent No. 6627794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AGAGGGCUGGUUAAGGCG 21
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ORGANISM: Artificial Sequence
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Best Local Similarity 63.2%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
APPLICANT: MARK, Hee Kyung
TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
FILE REFERENCE: PP05020/PCT
CURRENT APPLICATION NUMBER: US/09/980,052
CURRENT FILING DATE: 1999-05-29
PRIOR FILING DATE: 1999-05-29
PRIOR APPLICATION NUMBER: KR 10-1999-0019634
PRIOR APPLICATION NUMBER: KR 10-1999-0019634
PRIOR PILING DATE: 1999-05-29
PRIOR PILING DATE: 1999-05-29
PRIOR PILING DATE: 1999-05-29
PRIOR PILING DATE: 1999-05-29
PRIOR PILING DATE: 1999-06-29
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TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 9.1e+03;
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Pred. No. 9.1e+03;
3; Mismatches 4;
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US-08-520-313D-31/c
; Sequence 31, Application US/08520373D
; Patent No. 6451763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 51, Application US/09980052
Patent No. 6670130
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Chader, Gerald J
Becerra, Sofia P
Johnson, Lincoln V
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                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Tombran-Tink, Joyce
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                                                                                                                                                   OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 63.27
Matches 12; Conservative
                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.2
Matches 12; Conservative
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SOFTWARE: Kopatentin 1.71
SEQ ID NO 51
LENGTH: 20
NUMBER OF SEQ ID NOS: 501
SEQ ID NO 119
LENGTH: 20
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Search completed: October 16, 2006, 14:47:12 Job time : 56.5789 secs

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1: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
3: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
4: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
5: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
6: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
7: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
8: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
9: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
10: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
11: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
12: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
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18: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
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10: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
10: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
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11: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
12: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
13: FEMC_CELerra_SIDS3/ptodata/2/pubpna/USO0_PUBC
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Sequence 4341, App
Sequence 508384,
Sequence 510484,
Sequence 310484,
Sequence 310485,
Sequence 310486,
Sequence 534087,
Sequence 1286104,
Sequence 1286104,
Sequence 1286104,
Sequence 1286104,
Sequence 1286104,
Sequence 1286102,
Sequence 1286102,
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                                                                                                                               October 16, 2006, 14:16:09; Search time 337.985 Seconds (without alignments) 872.534 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-940-185-355

US-09-940-185-4341

US-09-940-185-4341

3 US-11-036-317-508584

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1 US-10-310-914A-310486

1 US-10-310-914A-310486

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US-10-310-914A-310487

US-10-310-914A-1266104

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Maximum Match 100%
Listing first 45 summaries
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24
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Match Length DB
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Perfect score:
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                                                                                                                                 Run on:
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| 18 | 15.2 | 63.3 | 25 | 15 | US-11-121-849-463132 | Sequence 470366, 25 | 15 | G2.5 | 25 | 9 | US-10-719-900-470366 | Sequence 470366, 25 | 15 | G2.5 | 25 | 13 | US-11-036-317-657262 | Sequence 657262, 25 | 13 | US-11-036-317-657262 | Sequence 657262, 25 | 13 | US-11-036-317-657262 | Sequence 657262, 25 | 14 | 15 | 62.5 | 25 | 13 | US-11-036-317-798014 | Sequence 731203, 25 | 14.8 | 61.7 | 21 | 11 | US-10-310-914A-75275 | Sequence 75275, 25 | 14.6 | 60.8 | 23 | 11 | US-10-310-914A-75275 | Sequence 75275, 27 | 14.6 | 60.8 | 23 | 11 | US-10-310-914A-75275 | Sequence 770100, 27 | 14.6 | 60.8 | 23 | 11 | US-10-310-914A-75275 | Sequence 770100, 27 | 14.6 | 60.8 | 24 | 11 | US-10-310-914A-75275 | Sequence 770100, 27 | 14.6 | 60.8 | 24 | 11 | US-10-310-914A-752432 | Sequence 770100, 27 | 14.6 | 60.8 | 25 | 13 | US-10-310-914A-752432 | Sequence 770100, 27 | 14.6 | 60.8 | 25 | 13 | US-10-719-956-115625 | Sequence 770100, 27 | 14.6 | 60.8 | 25 | 13 | US-10-719-956-115627 | Sequence 770100, 27 | 14.6 | 60.8 | 25 | 13 | US-10-719-956-115627 | Sequence 77 | Applitation of the condition of
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RESULT 1

US-11-036-317-713202/C

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ORGANISM: Artificial Sequence FEATURE:
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US-11-036-317-751276/c
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                                                                                                                                                                                                                                            67.5%; Score 16.2; DB 9; Length 25; 66.7%; Pred. No. 1.4e+03;
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 888593
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4341, Application US/09940185

Sequence 4341, Application US/09940185

Publication No. US20030096239A1

GENERAL INFORMATION:

APPLICANT: Cunderson, Kevin

APPLICANT: Cunderson, Revin

TITLE OF INVENTION: Probes and Decoder Oligonucleotides

FILE REFERENCE: A-69605-1

CURRENT APPLICATION NUMBER: US/09/940,185

CURRENT FILING DATE: 2001-08-27

PRIOR PILICATION NUMBER: US 60/228,854

PRIOR FILING DATE: 2000-08-29

PRIOR FILING DATE: 2000-08-29

PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 4768

SOFTWARE: Patentin version 3.1

SEQ ID NO 4341

LENGTH: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 365, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REPRENENE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR PILING DATE: 2000-08-25
; PRIOR PILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 365
: LENGTH: 24
                                                                                                                                                                                                                                                                                          Indels
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US-09-940-185-365
                                                                                                                                                                                                                                                                                                                                        4 GAGGGCUGGUUAAGGCGUCC 24
                                                                                                                                                                                                                                                                                                                                                                   23 GAAGGGCTAGTTAAGGCTTCC 3
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GAGAGGCGTTGGTTAAGGC 22
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                                                                                                                                                                                                                                                                                          14; Conservative
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Matches 14; Conservative
                                                                                                                                                                      ; ORGANISM: Mus musculus
US-10-719-900-888593
                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-09-940-185-365
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                     TYPE: DNA
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Sequence 751276, Application US/11036317

Sequence 751276, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REPRENCE: 3654, MBER: US/11/036,317

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2004-01-13

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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; Sequence 508584, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williama, Alan
; ATPLICANT: Williama, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; TILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION UNMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFURARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 508584
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; OTHER INFORMATION: Computer Generated Probe Sequence. US-09-940-185-4341
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Pred. No. 2.1e+03;
4; Mismatches 2;
                                                                                                                                              Query Match 65.8%; Score 15.8; DB 3; Best Local Similarity 73.7%; Pred. No. 2.1e+03; Matches 14; Conservative 3; Mismatches 2;
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68.4%;
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Best Local Similarity 68.4<sup>1</sup>
Matches 13; Conservative
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; ORGANISM: Mus musculus
US-11-036-317-751276
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US-10-914A-310486/c

US-10-914A-310486, Application US/10310914A

Sequence 310486, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION WUMBER: US/10/310,914A

CURRENT APPLICATION WUMBER: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: ParentIn version 3.3

SEQ ID NO 310486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 310487, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Biler, Kvuzat
APPLICANT: Biler, Kvuzat
APPLICANT: Biler, Wuzat
APPLICANT: Biler, Wuzat
APPLICANTON: Uses thereof
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 310487

LENGTH: 21
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                                                                                                                                                           Length 21;
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                                                                                                                                                                                                           Indels
                                                                                                                                                           63.3%; Score 15.2; DB 11; 75.0%; Pred. No. 4.1e+03; ive 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.2; DB 11;
Pred. No. 4.1e+03;
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75.0%; Pred. No. 4.1e+03;
tive 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.3%; Score 15.2; 75.0%; Pred. No. 4.1e+03; rive 2; Mismatches 3
                                                                                                                                                                                                                                                        1 UGAGAGGGCUGGUUAAGGC 20
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21 TGAGAGGGAAGGCTAAGGC 2
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; SOTTWARE: PatentIn version 3.3
; SEQ ID NO 310485
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.09
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.3
Best Local Similarity 75.0
Matches 15; Conservative
                                                                                                                                                                Query Match 63.3
Best Local Similarity 75.0
Matches 15; Conservative
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
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US-10-914A-310484/c
105-10-914A-310484/c
105-10-914A-310484, Application US/10310914A

Sequence 100484, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Kuaze

TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/310, 914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 310484
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US-10-914A-310485/c

US-10-310-914A-310485/c

Sequence 1310-915, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Kuzat

APPLICANT: Shiler, Kuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION UNDER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402
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                                                         Sequence 648052, Application US/11036317
Sublication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Best Local Similarity 63.6%; Pred. No. 2. (
Matches 14; Conservative 4; Mismatche
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US-11-036-317-648052/c
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; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-594065
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US-10-310-914A-1286104/c
; Sequence 1286104 Application US/10310914A
; Publication No. US2060003322A1
; Publication No. US2060003322A1
; GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: Uses thereof
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT PILLING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1286104
. LENGTH: 21
         Sequence 594029, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

APPLICANT: Bhiler, Kvuzat

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION UNMERE: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SEQ ID NO 594029

LENGTH: 21
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-112-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 21;
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US-10-310-914A-1056699/c
US-10-310-914A-1056699, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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Sequence 594065, Application US/10310914A

Sequence 594065, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich. Kvuzat

TITLE OF INVENTION:
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT PLING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402

SOFTWARKE: Patentin version 3.3

SEQ ID NO 594065

LENGTH: 24
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                                                                                                                                   Length 22;
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                                                                                                                               63.3%; Score 15.2; DB 11;
80.0%; Pred. No. 4.1e+03;
iive 1; Mismatches 3;
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Best Local Similarity 80.09
Matches 16; Conservative
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Best Local Similarity 85.0°
Matches 17; Conservative
; SEQ ID NO 1056699
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1056699
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Local Similarity
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US-11-217-529-25472
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88277, A
45581, A
111977,
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620818,
1233237,
74782, A
113852,
657889,
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32918, A
32919, A
32920, A
32921, A
620816,
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Sequence 25472, A
Sequence 101402,
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Sequence 792144,
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1. /EWC Celerra SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2. /EWC Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3. /EWC Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

4. /EWC Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

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5. /EWC Celerra_SIDS3/ptodata/2/pubpna/US1_NEW_PUB.seq:*

7. /EWC Celerra_SIDS3/ptodata/2/pubpna/US1_NEW_PUB.seq:*

8. /EWC Celerra_SIDS3/ptodata/2/pubpna/US1_NEW_PUB.seq:*

9. /EWC Celerra_SIDS3/ptodata/2/pubpna/US1_NEW_PUB.seq:*

9. /EWC Celerra_SIDS3/ptodata/2/pubpna/US1_NEW_PUB.seq:*

9. /EWC Celerra_SIDS3/ptodata/2/pubpna/US1_NEW_PUB.seq:*
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842.395 Million cell updates/sec
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                                                                                                                          October 16, 2006, 14:16:55 ; Search time 53.2331 Seconds
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                  GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-217-529-25472
US-11-217-529-36679
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-11-217-529-74782
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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Perfect score:
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25937, A
91282, A
112070,
125665,
135070,
136635,
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; Sequence 40910, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTONY LIMITED
; APPLICANT: NAKAWURA, VOSHIHIRO
; APPLICANT: ROJAWA, YUKIKO
; APPLICANT: KOJAWA, YUKIKO
; APPLICANT: ROJAWA, YUKIKO
; APPLICANT: TOWNKO
; APPLICANT: PUJIWIRA, TOWNKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT APPLICATION NUMBER: US 10/932,182
; PRIOR APPLICATION NUMBER: US 10/932,182
; RILNG DATE: 2004-09-02
; RNUMBER OF SEQ ID NOS: 197023
; SEQ ID NO 40910
; LENGTH: 25
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Publication No. US20060099612A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIWIRA, TOWOKO
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                             Sequence
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                         US-11-217-529-25937

US-11-217-529-1282

US-11-217-529-12565

US-11-217-529-125663

US-11-217-529-135070

US-11-217-529-136635

US-11-217-529-136635

US-11-348-413-130142

US-11-348-413-152231

US-11-348-413-152231

US-11-348-413-365681

US-11-348-413-365682

US-11-348-413-365682

US-11-348-413-365682

US-11-348-413-365682

US-11-348-413-365682

US-11-348-413-365682

US-11-348-413-365682

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US-11-348-413-365682
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Pred. No. 4.1e+03;
3; Mismatches 2;
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12; Conservative
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Query Match
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| Sequence 101402, Application US/11217529
| Publication No. US20060099612A1
| GENREAL INFORMATION:
| GENREAL INFORMATION:
| APPLICANT: SUNTORY LIMITED
| APPLICANT: NAKAWURA, NORIHISA
| APPLICANT: NAKAWURA, YOWOKO
| APPLICANT: KODAMA, YUKKO
| APPLICANT: KODAMA, YUKKO
| APPLICANT: FUVIMURA, TOWOKO
| TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
| TILE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
| CURRENT APPLICATION NUMBER: US/11/217,529
| CURRENT FILING DATE: 2005-09-02
| FRIOR PILING DATE: 2004-09-02
| NUMBER OF SEQ ID NOS: 197023
| SEQ ID NO 101402
| LENGTH: 25
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APPLICANT: NAKANO, YOSHIHIRO
APPLICANT: NAKANO, YOSHIHIRO
APPLICANT: NAKANO, YOSHIHIRO
APPLICANT: NAKANOMA, YUKIKO
APPLICANT: KODAWA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TILLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
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Pred. No. 6.3e+03;
4; Mismatches 6; Indels
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Pred. No. 6.3e+03;
4; Mismatches 1;
; FILE REFERENCE: S-38-285; CURRENT APPLICATION NUMBER: US/11/217,529; CURRENT FILING DATE: 2005-09-02; PRIOR APPLICATION NUMBER: US 10/932,182; PRIOR FILING DATE: 2004-09-02; NUMBER OF SEQ ID NOS: 197023; SOFTWARE: Patentin version 3.3; SOFTWARE: Patentin version 3.3; LENGTH: 25
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2-11-217-529-36679/c
; Sequence 36679, Application US/11217529
; Publication No. US2006009612A1
; GENERAL INFORMATION.
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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-25472
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Best Local Similarity 66.7%;
Matches 10; Conservative
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Best Local Similarity
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US-11-217-529-101402/c
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Murphy, Blen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: PCT/USOS/035471
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
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APPLICANT: Mounte, William M
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
PRIOR APPLICATION NUMBER: PCT/USOS/035471
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NAME/KEY: misc_feature
LOCATION: (1): (125)
OTHER INFORMATION: SEQ ID NO: 5316; WAN01UNLH_at; Start 930; Stop 954;
OTHER INFORMATION: 00001000000000
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66.7%; Pred. No. 7.8e+03;
tive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                            3, Mismatches
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GENERAL INFORMATION: APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 792144, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                          ; TYPE: DNA; CRCharomyces pastorianus US-11-217-529-36679
                                                                                                                                                                                                                                                                                                                                                                          3 AGAGGGCUGGUUAAGGC 20
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SOFTWARE: Patentin version 3.3
SEQ ID NO 8679
LENGTH: 25
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Matches 12; Conservative
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ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
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Best Local Similarity
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US-11-348-413-877012/c
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US-11-348-413-792144
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APPLICANT: NAKAO, YOSHIHED
APPLICANT: NAKAO, YOSHIHED
APPLICANT: NAKAO, YOSHIHED
APPLICANT: NAKAWURA, YOTKO
APPLICANT: KODAWA, YOTKO
APPLICANT: WINDING TOWN TOWN
THE OF INVENTY OF TWENTYON: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTHARE: PATENTIN VERSION 3.3
SOFTHARE: PATENTIN VERSION 3.3
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Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: FUJIMURA, YOKINISA
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKAI, YOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 5-38-285
                     TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                                                 Length 25;
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1. Similarity 57.1%; Pred. No. 9.6e+03;
12; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                              ch 54.2%; Score 13; DB 8; 1
1 Similarity 57.1%; Pred. No. 9.6e+03;
12; Conservative 4; Mismatches 5
                                                                CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-02-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 41374
LENGTH: 25
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CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
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Publication No. US2006009612A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   , ORGANISM: Saccharomyces pastorianus
US-11-217-529-41374
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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-88277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGTTGGGCTGGTTCAGGATTC 21
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Matches 12; Conserv
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NAME/KY: misc feature
LOCATION: (1). (25)
OTHER INFORMATION: SEQ ID NO: 7631; WANOIUMIA_at; Start 143; Stop 167;
OTHER INFORMATION: 000000011100000
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Publication No. US20060099612A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NAKAMINAL LIMITED
APPLICANT: NORAWINAL VUKIKO
APPLICANT: FUJIMINAL YOMKIKO
APPLICANT: FUJIMINAL YOMKIKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
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54.2%; Score 13; DB 8; Length 25;
Best Local Similarity 57.1%; Pred. No. 9.6e+03;
Matches 12; Conservative 4; Mismatches 5; Indels
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PRIOR FILING DALL.
PRIOR APPLICATION NUMBER: US L.,
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR PILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 877012
r.RNGTH: 25
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PRIOR FILING DATE: 2004-09-02
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Publication No. US20060099612A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Saccharomyces pastorianus US-11-217-529-29983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AGAGGGCUGGUUAAGGCGUC 23
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAWA, YOKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 29983
LENGTH: 25
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Publication No. US20060099612A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAWURA, NORIHISA
APPLICANT: NAKAWURA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: TUJIMURA, TUMKO
APPLICANT: TOSHIHIKO
FILE REPRENCE: S-38-285
CURRENT FILING DATE: 2005-09-02
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT APPLICATION NUMBER: US 10/932,182
PRIOR PILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PALENTIN Version 3.3
SEQ ID NO 111977
LENGTH: 25
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Publication No. US2060099612A1

GENERAL INFORMATION:

APPLICANT: SUNTORY LIMITED

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAO, YOSHIHIRSA

TILLE OF INVENTYON: WETHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: S-38-285

CURRENT FILING DATE: 2005-09-02

PRIOR PILING DATE: 2005-09-02

PRIOR APPLICATION NUMBER: US 10/932,182

PRIOR PELLING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 197023

SOFTWARE: Patentin version 3.3

SOFTWARE: Patentin version 3.3
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PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
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LENGTH: 25
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US-11-217-529-177967/c
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APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Onneted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REPERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: PCT/USOS/035471
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
RIOR FILING DATE: 2004-10-05
SRO ID NO 32918
LENGTH: 25
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APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Oldsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: PCT/USO5/035471
PRIOR FILING DATE: 2005-10-05
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LOCATION: (1)...(25)
OTHER INFORMATION: SEQ ID NO: 423; WANOIUJBU; Start 271; Stop 295;
OTHER INFORMATION: 1111111100000000
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                                                                                                Query Match 53.3%; Score 12.8; DB 8; Best Local Similarity 62.5%; Pred. No. 1.2e+04; Matches 10; Conservative 4; Mismatches 2;
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; Sequence 32918, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
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Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-177967
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Best Local Similarity 62.55
Matches 10; Conservative
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OTHER INFORMATION: probe
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RESULT 15
US-11-348-413-32920
Sequence 32920, Application US/11348413
Fublication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 32920
LENGTH: 25
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COTHER INFORMATION: probe
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1). (25)
COCATION: (21). (25)
COTHER INFORMATION: SEQ ID NO: 423; WANOIUJBU; Start 272; Stop 296;
COTHER INFORMATION: 111111100000000
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NAME/KEY: misc_feature

LOCATION: (1)..(25)

OTHER INFORMATION: SEQ ID NO: 423; WANOIUJBU; Start 273; Stop 297;

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US-11-348-413-32920
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PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 32919
LENGTH: 25
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Best Local Similarity 62.5
Matches 10; Conservative
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ORGANISM: Artificial
FEATURE:
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Hominidae; Homo.

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Mohapatra,S., Mohapatra,S., Yang,M., Ansari,A.A., Parronchi,P.,
Maggi,E. and Romagnani,S.
Molecular basis of cross-reactivity among allergen-specific human T
cells: T-cell receptor V alpha gene usage and epitope structure
Immunology 81 (1), 15-20 (1994)
AX996400 Sequence CQ874706 Sequence CQ874706 Sequence CQ37929 Remedy for AX390010 Hepatitis CQ149122 Sequence CQ3307710 Sequence CQ34455 Sequence CQ34455 Sequence AX177451 Mus muscu CQ546820 Sequence AX177451 Mus muscu CQ546820 Sequence AX177451 Mus muscu CQ546820 Sequence AX1737 Human RET p CQ630945 Sequence AX39773 Mesocrice AX907922 Sequence AX907925 Sequence AX907925 Sequence AX907947 Sequence AX907944 Sequence AX9735208 Sequence AX735208 Sequence
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Homo sapiens T-cell receptor alpha-chain (TcR V alpha) mRNA,
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/note="allergen-specific; mismatch(30[D->N]) when compared
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Homomalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 144559] from the original journal article.
Location/Qualifiers
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/mod_type="mRNA"
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/protein_id="AAB30241.2"
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CQ34710
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BF012636
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                              AX390010
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S69137/c
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   ORIGIN
                                                                // Search time 1370 Seconds
(without alignments)
11762.591 Million cell updates/sec
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Sequence
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S69198 Homo sapien
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AX184498 Sequence
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AY751306
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           GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                    6366136 seqs, 31973710525 residues
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Maximum Match 100%
Listing first 45 summaries
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AR150733
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AR735995
CQ441292
CQ480460
AR751306
AR431314
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AR606335
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AB150733.1 GI:62171551
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                                                                                                           Hominidae; Homo.
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                                                      Homo sapiens
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1 (bases 1 to 98)
Mohapatra, S. S., Mohapatra, S., Yang, M., Ansari, A.A., Parronchi, P., Maggi, E. and Romagnani, S.
Molecular basis of cross-reactivity among allergen-specific human T cells: T-cell receptor V alpha gene usage and epitope structure immunology 81 (1), 15-20 (1994)
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Номо sapiens T-cell receptor alpha-chain (TcR V alpha) mRNA,
partial cds.
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                                                                                        65 GTTTTCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAGG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 144557] from the original journal article. Location/Qualifiers
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/product="T-cell_receptor_alpha-chain"
/protein_id="Mab30239.2"
/protein_id="Mab30239.2"
/tanslation="DSATYPCAASTTNAGKSTFGGGTTLTVKPNIQ"
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/mol_type="mRNA"
/dolate="slase sensitive individual VI 17"
/do_xref="taxon:9606"
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                   Length 98;
                                                      37; Indels
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                  Score 27.8; DB 5;
Pred. No. 1.9e+03;
0; Mismatches 37;
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Pred. No. 6.2e+03;
0; Mismatches 38
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                  th 11.0%;
| Similarity 57.5%;
| So, Conservative
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Homo sapiens
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Matches 49; Conserva
                                    Best Local Similarity
Matches 50; Conserv
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AB150733
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Tamiya,G., Makino,S., Fujimoto,K., Oka,A., Hayashi,H., Denda,A., Linsen,S.E., Ikuta,T., Shinya,M., Endo,T., Tomizawa,M., Tokubo,E., Sato,R., Takaki,A., Nagateuka,Y., Watanabe,H., Adachi,S., Makino,Y., Nakano,S., Yamamoto,A., Yoshida,K., Okamoto,K., Yamaguchi,D., Yamaguchi,B., Yamamoto,A., Yoshida,K., Okamoto,K., Yamaguchi,D., Ishibashi,H., Yonekura,M., Takayama,S., Nakami,Y., Saruwatari,T., Barad,A., van Hilten,J.A., van de Watering,L.M., Giphart,M.J., Bahram,S., Kulski,Y.J. and Inoko,H.

Direct Submission

Submitted (12-DEC-2003) Hidetoshi Inoko, Tokai University School of Medicine, Department of Genetic Information; Bohseidai, Isehara, Kanagawa, 259-1193, Japan (E-mail:hinoko@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121, Fax:81-463-94-8884)

Polymorphisms were confirmed by comparing with the pooled DNA typing data of 8B Dutch population or 100 Australian. When there was no significant difference between the Japanese and these Caucasians, individual typing was performed to confirm
                                                                                                                                                                                                              Tamiya,G., Shinya,M., Imanishi,T., Ikuta,T., Makino,S., Okamoto,K., Furugaki,K., Matsumoto,T., Mano,S., Ando,S., Nozaki,Y., Yukawa,W., Nakashige,R., Yanaguchi,D., Ishibashi,H., Yonekura,M., Nakami,Y., Takayama,S., Endo,T., Saruwatari,T., Yagura,M., Yoshikawa,Y., Fujimoto,K., Oka,A., Chiku,S., Linsen,S.E., Giphart,M.J., Shilaki,J.K., Fukazawa,T., Hashimoto,H., Kimura,M., Hoshina,Y., Shilaki,Y., Hotta,T., Wondi,M., Mincaki,T., Komai,K., Shiozawa,S., Taniguchi,A., Yamanaka,H., Kamatani,N., Gojobori,T., Bahram,S. and Inoko,H.
Mhole genome association study of rheumatoid arthritis using 27 039 microsatellites
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/PCR conditions="denaturation 96degC 5 min, 57degC 1 min, 72degC 1 min, 40 cycles 96degC 45 sec, 57degC 1 min;
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/note="pooled DNA of 100 Japanese unrelated individuals
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/note="sequence tagged site D10S08121"
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/db_xref="taxon:9606"
/chromosome="10"
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complement(89. .109)
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sapiens (human)
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PAT 18-DEC-2003
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schlegel, R., Endege, W.O. and Monahan, J.E. Genes differentially expressed in human prostate cancer and their
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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156 CAGCTCGCAGTCGGCCAGGGAGGCGGGGAGAGACGAGCGGCTCTGGCCCC 207
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                      156 CAGCTCGCAGTCGGCAGGGAGGGCGGGGGAGAGACGAGCGGCTCTGGCCCC
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9.8%; Score 24.8; DB 2;
Best Local Similarity 67.3%; Pred. No. 1.7e+04;
Matches 35; Conservative 0; Mismatches 17;
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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                                                                                                                    Sequence 16064 from Patent EP1033401. AX900201
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Sequence 3158 from Patent WO0160860.
CQ471292
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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1 (bases 1 to 92)

2 (Badards, J.B.D.M., Duclair, E. and Jordan, J.Y.

Sequence tag and encoded human protein

Patent: JP 2001269182-A 11980 02-OCT-2001;
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24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
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Pred. No. 1.7e+04;
0; Mismatches 17; Indels
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Edwards, J.-B.D.M., Duclert, A. and Giordano, J.-Y.
Expressed acquence tags and encoded human proteins
Patent: US 6783961-A 16064 31-AUG-2004;
Genset S.A.;;
                                                   linear
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                                          Sequence tag and encoded human protein.
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Sequence 16064 from patent US 6783961.
AR735995
AR735995.1 GI:77429735
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/db_xref="taxon:9606"
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/organism="unknown"
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JP 2001269182-A/11980
                                                                                                    BD035734.1 GI:22577476
JP 2001269182-A/11980.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 67.3%;
Matches 35; Conservative
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Method, array and kit for detecting activated transcription factors
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                                                                                                                                                                                                                                             37 CCCCAAGTTGGAAGGGCGCTTTTGTTTTTTTTGGATGCAGGTCCTCTGACTCCCTC 96
                                                                                                                                                                                                                                                                                 9 ceccrretrierreseseacresecerrirarcrereseceaseasireseseasianes
         fiseue_type="herpetic skin lesion"
<1. .>13
<1. .>14
fiseue_type="herpetic skin lesion"
<1. .>15
forduct="T cell receptor beta chain"
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/db_xxef="GI:5A111803"
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Han, K., Kim, D. and Kim, H.-J.
Vector-based method for visualizing secondary structure of RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 GGCGTCCCCAAGTTGGAAGGGCGCTTTGCTTCTTGTTTTCTGGATGCAGAGTCCTCTGACT
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                                                                                                                                                                       9.7%; Score 24.4; DB 5; Local Similarity 54.4%; Pred. No. 2.4e+04; tes 49; Conservative 0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent: US 6651010-A 1 18-NOV-2003;
INHA University Foundation; Inchon-8i;
KRX;
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Sequence 145 from patent US 6696256.
AR477180.
AR477180.1 GI:47234454
                                                                                                                                                                                                                                                                                                                         97 IGCCACGGGCIGAGITICCGGCICCAGGIT 126
                                                                                                                                                                                                                                                                                                                                              1. .96
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                AR431314 96 bp
Sequence 1 from patent US 6651010.
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1 (bases 1 to 78)
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AR477180/c
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AR431314
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Homo sapiens clone RW33 T cell receptor beta chain mRNA, partial
                                                                                      PAT 30-JAN-2004
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I bases; I to 119)

Barcy, S., Huang, M.L., Corey, L. and Koelle, D.M.

Longitudinal Analysis of Herpes Simplex Virus-Specific CD4+ Cell Clonotypes in Infected Tissues and Blood

J. Infect. Dis. 191 (12), 2012-2021 (2005)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 GGAGGGCGGGGGAGGAGGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGT
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                                                                                        linear
                                                                                                                                                                                                                                                                                                                                          Patent: WO 0160860-A 12327 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
                                                                                    CQ480460 10327 from Patent WO0160860.
CQ480460

    .104
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/organism="Homo sapiens"
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62 CTCTTCCTTCGCTAACGCC 80
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AY751306.1 GI:54111802
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PAT 27-AUG-2002

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C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
                                                                                                                                                      109 AGTITICOGGCTCCAGGTTCGCGTGTCGCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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JP 2001269182-A/10981
24-PEB-2000
JP 200118773
26-PEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, BIMERIC DUCLAIR, JEAN YVES
                                                                                 Query Match
9.4%; Score 23.8; DB 2; Length 78;
Best Local Similarity 59.7%; Pred. No. 3.5e+04;
Matches 40; Conservative 0; Mismatches 27; Indels
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1 (bases 1 to 72)

Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y. Sequence tag and encoded human protein

Patent: JP 2001269182-A 10981 02-OCT-2001;
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Sequence 15065 from patent US 6783961.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1. .78
/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                            BD034735.1 GI:22576477 JP 2001269182-A/10981. Homo sapiens (human) Homo sapiens
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AR734996.1 GI:77428736
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Best Local Similarity
Matches 32; Conserv:
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PC C12P7-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 AGTITICCGGCTCCAGGITCGCGTGTCGCCTGAGGTTTGAGGCCCAGACAGCTCGCAGTCG 168
                                                                                                                                                                                                                              Method and kit for isolating DNA probes that bind to activated transcription factors
Patent: US 6924113-A 145 02-AUG-2005;
Panomics, Inc.; Redwood City, CA
Location/Qualifiers
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Method for screening for drug canusaction factor activity
transcription factor activity
Patent: US 6821737-A, 145 23-NOV-2004;
Panomics, Inc.; Redwood City, CA
Location/Qualifiers
Patent: US 6696256-A 145 24-FEB-2004;
Pandmics, Inc.; Redwood City, CA
Location/Qualifiers
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Sequence 145 from patent US 6821737.
AR606935.1 GI:56659110
                                                             /organism="unknown"
/mol_type="genomic DNA"
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PAT 11-OCT-2005

linear

Gaps

Search completed: October 16, 2006, 13:38:02 Job time : 1373 secs

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27-MAR-2003 (first entry)
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GenCore version (c) 1993 - 2006
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Listing first 45 summaries
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	ABQ76940	standard;	DNA;	115	BP.	
AC AB	ABO76940;					

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Polylinker Scal-Li-(Bsgl-Scal) DNA

Murine, T cell receptor; TCR; hdm2; T cell response; alpha TCR; beta TCR; antigen-recognising sequence; ARS; fusion construct; cytostatic; apoptotic; tumour; leukaemia; immunisation; ds.

01-MAR-2001; 2001DE-01009854

01-MAR-2001; 2001DE-01009854

Stanislawski

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New polypeptide of a murine alpha/beta T-cell receptor, useful for treating tumors and leukemia, induces specific lysis or apotosis of cells expressing hdm2 protein.

Example 2; Fig 6; 52pp; German.

This invention describes a novel murine alphabeta T-cell receptor (TCR) that mediates a hdm2 protein-specific T cell response, a fusion protein (FP) that includes the TCR and nucleic acid encoding it, alpha or betachains of a TCR that include the antigen-recognizing sequence (ARS) of an

expression and secretion vectors

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antibody specific for aa 81-88 of hdm2 (or its complex with HLA-A2-specific antibody) and a method for identifying hdm2-specific antigens. The TCR of the invention has cytostatic and apoptotic activity. The products of the invention are useful for treatment, prevention and diagnosis of hmd2-associated diseases, particularly tumours and leukaemia, including use for passive or active immunisation. They can also be used to screen for therapeutic agents. This sequence encodes the polylinker Scal-Li-(Bsgl-Scal) fragment used in the construction of the fusion constructs described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTS are derived from mNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 CTGAGTTTCCGGCTCCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAG 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                               Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                         Gaps
                                                                                                                                           156 CAGCICGCAGICGGGCAGGGCGGGGAGAGACGAGCGGGCTCTGGCCCC 207
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                                                                     Length 92;
                                                                                                       17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 103 BP; 9 A; 38 C; 30 G; 26 T; 0 U; 0 Other;
                                 Sequence 92 BP; 19 A; 24 C; 44 G; 5 T; 0 U; 0 Other;
                                                                 Query Match
9.8%; Score 24.8; DB 3;
Best Local Similarity 67.3%; Pred. No. 2.1e+03;
Matches 35; Conservative 0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                               Human prostate expression marker cDNA 3158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 581; 11750pp; English.
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16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-UUN-2000; 2000US-021314P.
18-JUL-2000; 2000US-0219007P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                             13-SEP-2002
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62 CTCTTCCTTCGCTAACGCC 80

(first entry)

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Human; colon cancer, colon cancer antigen; diagnosis; detection;
                                                                                                                                      Human colon cancer antigen encoding cDNA SEQ ID NO:3242.
                                                                                                                                                                                                                                                                         28-SEP-2000; 2000WO-US026524.
                                                            AAH36160 standard; cDNA; 105
                                                                                                                                                                           colorectal carcinoma; ss.
                                                                                                                                                                                                                          WO200122920-A2
                                                                                                                                                                                                  Homo sapiens
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                                                                                                             03-SEP-2001
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                                                                                      AAH36160;
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              61
                                                                                                                                                                                                                        Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patis; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
9.8%; Score 24.6; DB 5; Length 104; 57.0%; Pred. No. 2.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 104 BP; 9 A; 39 C; 30 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                 Human prostate expression marker cDNA 12327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monahan JE;
                                     234 CTCTCCTTTCGCCACCTCC 252
                                                                                                                         ABV12336 standard; cDNA; 104 BP
                                                            62 crcrrccrrccracccc 80
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09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
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2000US-0189862P.
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                                                                                                                                                                          (first entry)
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99US-0157137P.

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cancer-associated nucleic acid molecules (N) and proteins (P), where the cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diagnosis and vaccine production. N and P may be used in the prevention, diagnosis cample, N and P may be used to treat diaorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that ffect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids to produce the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AMH37196 to AMH37204 and AMB7789 represent sequences used in the exemplification of the present invention. N. B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
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                                                                                                                                                        Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 5034-5035; 9803pp; English ..
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                                                                                                                                                        Birse CE,
(HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                        Barash SC,
                                                                                                                                                                                                                                                                                                         WPI; 2001-235357/24.
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                                                                                                                                                        Ruben SM,
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174 GGAGGGGGGGGAGAGACGAGCGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGT 233

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Indels

34;

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45; Conservative

Best Local Similarity Matches 45; Conserv

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Query Match

234 CTCTCCTTTCGCCACCTCC 252

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises a method for identifying complexes between a transcription factor and another protein. The invention also comprises a method for isolating DNA probes which bind to activated transcription factors. The methods of the invention are useful for identifying transcription factor-protein interactions. The methods of the invention are also useful for facilitating the screening and identification of new drugs, characterising their mechanism of action and screening for adverse side effects based on drug's impact expression. The present DNA sequence represents a probe used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                     Identifying transcription factor-protein complexes, by isolating transcription factor complexes from sample based on a specific type of factor, and identifying different proteins present in isolated complexes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 AGTITICCGGCTCCAGGTICGCGTGTCGCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription factor-related array hybridisation probe - SEQ ID No 145
                                                                                                       Probe; 88; transcription factor-protein complex; transcription factor; drug screening; drug identification; array hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 9.4%; Score 23.8; DB 8; Length 78; 1 Similarity 59.7%; Pred. No. 3.98+03; 40; Conservative 0; Mismatcher 27. Thank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 78 BP; 15 A; 27 C; 15 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein 5' EST, SEQ ID NO: 15065.
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 6; 167pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Βb
                     ABT17318 standard; DNA; 78 BP.
                                                                                                                                                                                                                        08-JUN-2001; 2001US-00877243.
08-JUN-2001; 2001US-00877403.
08-JUN-2001; 2001US-00877705.
08-JUN-2001; 2001US-008477738.
05-SEP-2001; 2001US-00947274.
                                                                                                                                                                                                      30-MAY-2002; 2002WO-US017408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC10990 standard; cDNA; 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                               (first entry)
                                                                                                                                                                                                                                                                                          (PANO-) PANOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 GGCAGGG 175
                                                                                                                                                                                                                                                                                                                                  WPI; 2003-148829/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCAGAG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 40; Conserv
                                                                                                                                                             WO2002101351-A2
                                                              10-APR-2003
                                                                                                                                         Unidentified
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                                                                                                                                                                                  19-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
                                          ABT17318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC10990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
RESULT 7
AAC10990/C
1D AAC10
XX
AC AAC10
XX
DT 06-0C
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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 GCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCGGGCAG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 15065; 71pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ecergeseccesesarcsásecarccáscacacadaseces 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 72 BP; 9 A; 33 C; 20 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cervical cancer marker nucleic acid 193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                               21-FEB-2000; 2000EP-00200610.
                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0122487P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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nes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEST ) GENSET
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                                                                                                                                                                                                  EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1999;
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containing many identical probes. The probes are nucleotide species of the containing many identical probes. The probes are nucleotide sequences of 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at least one includes a segment of at least 20 bases identical with, or complementary to, a segment of an open reading frame (orf) of Escherichia coli K12. The biochip is used for specific detection of gene expression in K12 and for determining the gene expression pattern, e.g. for diagnostic determination of which E. coli strains are present in the biochip provides as comprehensive as prosection of expression. The biochip provides as comprehensive as present in the such and to determine the effects of e.g. growth media on gene expression. The biochip provides as comprehensive as pressible detection of the K12 genome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or
                                                                                                                                                                                                                                                                                                                                                    other B. coil strains in a single experiment. Apart from qualitative and quantitative information about gene expression, it also allows measurements of population densities for the various strains. The use of synthetic oligomucleotides for preparation of probes allows free variation in probe length and ensures high purity (and thus selectivity, eactivity, and reproducibility); also synthetic probes are generally shorter than probes prepared by probes are generally chosent than probes of probes are generally shorter than probes of probes are generally shorter than probes of probes are generally shorter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochip containing probes complementary with open reading frames in
Escherichia coli Kl2, useful for detecting gene expression and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel biochip comprising probe spots, each containing many identical probes. The probes are nucleotide sequences of 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at least one includes a segment of at least 20 bases identical with, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 CACGGGCTGAGTTTCCGGCTCCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGAC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 caagirichgegeegeergeacearganginegesagesageegeegerrichgeeages 32
                                                       This invention describes a novel biochip comprising probe spots,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochip; gene expression; gut; diagnostic; detection; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 100 BP; 21 A; 29 C; 38 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.4; DB 8;
Pred. No. 5.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. coli K12 MG1655 biochip probe SEQ ID 7863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weber J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 1228; 2004pp; German.
       Claim 3; Page 168; 2004pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-2001; 2001EP-00112179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACD76587 standard; DNA; 100
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Best Local Similarity 63.2
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1260592-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 GACGAGCGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGTCTCTCTTTCGCCAC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochip containing probes complementary with open reading frames in Escherichia coli K12, useful for detecting gene expression and expression
                                                                                                                                                                                                                                                                                                          and treating cervical cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    progression of cervical cancer or a premalignant condition in a patient, and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
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                                                                                                                                                                                                                                                                                                                                  for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4%; Score 23.6; DB 4; Length 97;
59.4%; Pred. No. 4.8e+03;
ive 0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 97 BP; 7 A; 34 C; 30 G; 23 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E. coli K12 MG1655 biochip probe SEQ ID 1015.
                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                        New isolated nucleic acid for diagnosing
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 137; 1051pp; English
                                                                                                                                                                                                       Berger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huber A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACD69745 standard; DNA; 100 BP.
21-DEC-1999; 99US-0171350P.
14-WAR-2000; 2000US-0189135P.
12-WAY-2000; 2000US-0203791P.
09-UTM-2000; 2000US-0210600P.
21-JUL-2000; 2000US-0220114P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MWGB-) MWG-BIOTECH AG.
                                                                                                                                                                                                       Deeds J,
                                                                                                                                                                                                                                                         WPI; 2001-375006/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 CTCC 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1260592-A1
                                                                                                                                                                                                       Schlegel R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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ACD69745/ RESULT 9

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0; Gaps

21; Indels

Length 100;

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complementary to, a segment of an open reading frame (orf) of Escherichia coli K12. The biochip is used for specific detection of gene expression in K12 and for determining the gene expression pattern, e.g. for diagnostic determination of which E. coli strains are present in the gut, and to determine the effects of e.g. growth media on gene expression. The biochip provides as comprehensive as possible detection of the K12 genome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or other E. coli strains in a single experiment. Apart from qualitative and quantitative information about gene expression, it also allows measurements of population densities for the various strains. The use of synthetic oligonucleotides for preparation of probes allows free variation in probe length and ensures high putity (and thus selectivity, exectivity and reproducibility); also synthetic probes are generally shorter than probes prepared by polymerase chain reaction. ACD68731 to ACD8550 represent oligonucleotide probes used with the biochip described
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Sequence 100 BP; 13 A; 35 C; 29 G; 23 T; 0 U; 0 Other;

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                                                                 100 CACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGAC 156
                                                                                         CAAGTICTGCGCCGCCTGCACCTTCGCCAGTGCCGCGCGCGGCTTTCTGGCCAGCC 99
                                     Gaps
                                     ö
Score 23.4; DB 8; Length 100;
Pred. No. 5.5e+03;
0; Mismatches 21; Indels C
 9.3%;
                                     36; Conservative
                      Local Similarity
                                                                                                   43
      Query Match
                                     Matches
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Oligonucleotide DmetER, SEQ ID 9. ADR28210 standard; DNA; 100 BP (first entry) 04-NOV-2004 ADR28210; RESULT 11 

2-amino-4-alkylthio-butyric acid; methionine synthase; cystathionine-gamma-synthase; as.

Synthetic.

FR2851255-A1. 20-AUG-2004. 14-MAY-2003; 2003FR-00005768

18-FEB-2003; 2003FR-00001924

(META-) METABOLIC EXPLORER

B, Soucaille PNP; Gonzales Chateau M,

WPI; 2004-618123/60.

acid, useful for preparing L-methionine, from simple carbon source and mercaptan or its salt, have modified methionine synthase activity. strains of microorganisms that produce 2-amino-4-alkylthio-butyric

Example 1; SEQ ID NO 9; 68pp; French.

The present invention relates to a novel strain (A) of a microorganism which produces a 2-amino-4-alkylthio-butyric acid (I) by metabolising a simple sugar and a thiol (II), or its salt, and has at least one gene encoding an enzyme with modified methionine synthase (MS) activity. (A) are specifically used for fermentative production of L-methionine, which synthesis of L-Met is independent of synthesis of Cysteine; the methyl mercaptan used is a toxic waste product from the petrochemical industry and synthesis of L-Met occurs in a single step from O-(acetyl or

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succinyl)-L-homoserine. The enzyme with modified MS activity is either cystathionine-gamma-synthase or an acylhomoserine sulfhydrylase, and is modified so that the substrate is reacted with (I) rather than with L-cysteine, to result in preferential conversion of the substrate to (I) or homocysteine. The present sequence was used in an example from the
                                                                                                                                                                                                                                                                                                                                        100 cacceccicacitrccecrccacerrcccrcrcrcrcrcrcrcrcrcrcacerrrcaceccacac 156
                                                                                                                                                                                                                                                                                                                                                                                CAAGTICTGCGCCCTGCACATGTTCGCCAGTGCCGCGCGCGCGTTTCTGGCCAGCC 68
                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                  ch 9.3%; Score 23.4; DB 13; Length 100; 1 Similarity 63.2%; Pred. No. 5.5e+03; 36; Conservative 0; Mismatches 21; Indels 0.
                                                                                                                                                                                        Sequence 100 BP; 15 A; 36 C; 25 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                             invention
                                                                                                                                                                                                                                             Query Match
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          88888888888
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BB; microorganism evolution; metabolic pathway; metabolite;
blotransformation; NADPH-dependent enzyme; nucleic acid metabolism;
lipid metabolism; sugar metabolism. Soucaille PNP, Chateau M, Gonzalez B, Meynial-Salles I, 17-FEB-2004; 2004WO-FR000354. 18-FEB-2003; 2003FR-00001924. 14-MAY-2003; 2003FR-00005768 14-MAY-2003; 2003FR-0005769 06-NOV-2003; 2003FR-00013054 (META-) METABOLIC EXPLORER WO2004076659-A2. 10-SEP-2004. 

Nucleic acid DmetER to generate evolved microorganisms.

(first entry)

02-DEC-2004

ADR99734;

ВР

ADR99734 standard; DNA; 100

ADR9973

New evolved microorganisms with altered metabolic pathways, useful e.g for production of amino acids, are selected as mutants able to grow on zink O; WPI; 2004-653418/63

Disclosure; SEQ ID NO 1; 113pp; French.

defined media.

The invention relates to a method for preparing evolved microorganisms

(A) with modified metabolic pathways comprising: (a) genetic modification

of a microorganism to inhibit production or consumption of a metabolite

when it is grown on a defined medium, thus affecting its ability to grow,

the modified organism in the defined medium so that evolution;

and (c) selecting as (A) cells able to grow on the medium, optionally in

presence of co-substrate. The evolved microorganisms (A), or evolved

processes, especially those involving NADPH-dependent enzymes,

processes, especially those involving NADPH-dependent enzymes,

also synthesis of amino acids (Met, Cys, Thr, Lys or Ile) but

also synthesis of nucleic acids or lipids, and metabolism of sugars. (A)

provide more efficient production of selected metabolites than parent

strains. This sequence represents a nucleic acid molecule used in the

method of the invention.

(first entry)

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Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                     Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                      Human bone marrow expressed single exon probe SEQ ID NO: 19144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO 19144; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000US-00608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2000; 2000US-0236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-2000; 2000US-0234687P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                       WO200157276-A2
                                                                                                                                                                                                                                             Homo sapiens.
                                                                          06-NOV-2001
                                                                                                                                                                                                                                                                                                                                      09-AUG-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG,
                             AAK44587;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; brain; nerve degeneration; nootropic; neuroprotective; antiporvulsant; antiparktinsonian; antidorvulsant; infarction; Parkinson's disease; Alzheimer's disease; Huntington's disease; muscular hypoplastic lateral sclerosis; diabetic neuropathy; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New protein isolated from human embryonic brain useful for treating nerv
degeneration diseases e.g. Parkinson's diseases and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (I) which has nootropic, neuroprotective, anticonvulsant, antiparkinsonian and antidiabetic activity. (I) is useful for treating nerve degeneration diseases e.g. Parkinson's disease, Alzheimer's disease, muscular hypoplastic lateral sclerosis, Huntington's disease, brain infarction, diabetic neuropathy and traumatic nerve degeneration. AAZ89256-Z89234 represent PCR primers used in the isolation and amplification of the human brain protein described in the method of the
                                                                                                                                          100 CACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGAC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel human embryonic brain derived protein
                                                                                                                                                                                            68
                                                                                                Gaps
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                                          Score 23.4; DB 13; Length 100;
Pred. No. 5.5e+03;
0; Mismatches 21; Indels 0
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  Sequence 100 BP; 15 A; 36 C; 25 G; 24 T; 0 U; 0 Other;
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Pred. No. 5.5e+03;
0; Mismatches 18;
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                                            9.3%;
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                                                                     Local Similarity 63.2
les 36; Conservative
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Chen W, Rank DR;

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 GTTAAGGCGTCCCCAAGTTGGAAGGCGCTTTGCTTCTGTTTTCTGGATGCAGAGTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 101 BP; 36 A; 22 C; 23 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK18659 standard; DNA; 101
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Gaps

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18; Indels

Local Similarity 65.4 1es 34; Conservative

Matches

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CTCGCAGTCGGGCAGGGCGGGGGGAGAGACGAGCGGCTCTGGCCCCTTA 210

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AAK44587 standard; DNA; 101 BP

RESULT 14
AAK44587/C
ID AAK44

09-AUG-2001

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human brains.
                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO 18650; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.2; DB 4; Length 101;
Pred. No. 6.3e+03;
0; Mismatches 23; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 101 BP; 36 A; 22 C; 23 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                          Penn SG, Hanzel DK, Chen W, Rank DR;
                                                               04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053266.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02346359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.2%;
Best Local Similarity 61.7%;
Matches 37; Conservative 0
                                30-JAN-2001; 2001WO-US000667
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Search completed: October 16, 2006, 13:14:41 Job time : 257 secs

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Gaps ô

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Sequence:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

E 1 (bases 1 to 100)
S Dum, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Rallam,H., Longacre,S., Mahmoud,M., Mesenn,E., Pedersen,T., Rellam,H., Longacre,S., Mahmoud,M., Mesenn,E., Pedersen,T., Niederhausern,A. and Wright,D.,Weiss,R. Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Tingey,A., von Dyaemid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
CN071764 1021018H1
CW171487 104 493 1
DU188381 109857418
BZ288533 3590_1 36
CK005996 33821181C
CL952595 OGIRUAO01
CL952595 OGIRUAO01
CK951897 907470 MA
CK71897 907470 MA
CK7100624 CC57742.5
BJ965732 BJ9657328
BJ965777 BJ965717
BJ970068 BJ970068
BJ967752 BJ967752
AW6131414 7468 MARC
BJ564385 BJ554385
AM93199 UI-M-BH3-AZ922634 SLCCC2D11
CN868873 001202AAO
CCO18108 EST788499
BG994249 CM3-HT115
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1M0570K16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0570K16 F, genomic survey sequence.
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84112, USA
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Insert Length: 10000 Std Error: 0.00
Plate: 0570 row: K column: 14
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="tutc:imos70k16"
/sex="Male"
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Seg primer: CGTYCTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 100.
Location/Qualifiers
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     CW11764
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CL952595
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BJ965328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ769498.1 GI:12889695
          Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@geneti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .100
       Mus musculus
        \begin{array}{c} \mathbf{v} \bullet \mathbf
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     source
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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COMMENT
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AZ769498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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CG574657 OST20730
CG535738 OST120730
CK014560 33148FE1C
CL952591 OSTRUAN01
AV847732 AV81732
DU408432 109847402
CG255380 OGVCP92TH
AV800261 MR2-UM006
DV900899 POSM06050
AX657609 RPCT-23-2
BZ97609 RPCT-23-2
BZ9170 CH240_225
AL182961 TETEAGON
GEST600 AX80011.
BZ987103 TETEAGON
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DV552589 2E12.dat
DN773586 E1235 [C1
                                                                                                                                                                             ; Search time 2284 Seconds (without alignments) 6169.734 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                1 gggttatctgcaactgagag......tctctcctttcgccacctcc 252
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                                 GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1484138
                                                                                                                                                                                                                                                                                                                                                                                                                                                          48236798 seqs, 27959665780 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fotal number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                              nucleic search, using sw model
                                                                                                                                                                               October 16, 2006, 13:38:19
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CC014560
CL952591
AV841732
DIJ408432
CG255380
AW800261
DV900899
AZ697609
BG718505
BZ836170
CNS02660
CRS02660
CRS02660
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DV552589
DN773586
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                                                                                                                                                                                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                             US-10-604-726A-8797
252
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11
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
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Minimum DB Maximum DB

Database

Searched:

GSS 16-FEB-2001

5

00000

Result 8

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LOCUS CK014560 110 bp mRNA linear EST 04-FEB-2005 DEFINITION 33148rsicef_6492.yl Oryza sativa cv. PA648 panicle sterile cDNA
                                                                                                                                                                                                                                                                                                                                                                                                         CG535738 82 bp mRNA linear GSS 01-OCT-2003 OST122945 Mus musculus 1295v/Ev Mus musculus cDNA clone OST122945,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene Trap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 TGTTTTCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGCTGAGTTTCCGGCTCCAG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Sampronic, Abuin, A., Ramirez-Solis, R., Richter, L.J., Ambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B. W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparke, M.J., Wan Sligtenhorst, I., Yogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.
Whi kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                          39 CCAAGTIGGAAGGGCGCTITIGCTICTGTTITCTGGAIGCAGAGTCCTCTGACTCCCTC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 İGİTİTİTİĞICNCÇAAAĞATÇİÇİÇANAÇAÇİTAĞCAÇCAAÇIAGGCANCNTAÇNCÇAĞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
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                                                                                          Length 103;
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                                                                                                                                                Indele
/clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
                                                                                       Score 27.6; DB 12;
Pred. No. 8e+03;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="OST122945"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: materials@lexgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
CG535738
CG535738.1 GI:37322310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Zambrowicz BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 GTTCGCGTGTCGCCCT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
                                                                                       Query Match
Best Local Similarity 67.2%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 CTTGATATGAGGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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CK014560/c
                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
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                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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                                    ORIGIN
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                                                                                                                                                                     was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymurclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWM92 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM Mus musculus
Eukaryota; Macazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Muscidea; Muridae; Musina;
Sciurognathi; Muscidea; Muridae; Musina;
Butonica; B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Sambrowicz,B.P., Abuin,A., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorse,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Whill kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
D 14610273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG574657 103 bp mRNA linear GSS 02-OCT-2003 OST207730 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST207730,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9,392(6676):608-11) Class: Gene Trap.

Location/Qualifiers
                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA
   /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 GAGGCCAGACAGCTCGCAGTCGGGCAGGGAGGGCGGGGGAGAGACGAGGCGGCT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 écedecadercadecerrecedecededadadecededadadecededer 75
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.5%; Score 29; DB 11; Length 100; 71.7%; Pred. No. 3.38+03; 1ive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="OST207730"
/cell_type="embryonic stem cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CG574657
CG574657.1 GI:37364994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
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RESULT 2

65

FEATURES

TITLE

COMMENT

Gaps

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Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona, Phlebobranchia, Cionidae; Ciona.

1 (bases 1 to 99)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Norl Satoh
Department of Zoology
Kyoto University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 CGCCAGCCCGCCTTCAGCTTGAGGCCCCACATGGCCGTGCCGCGCGGGAGATGGGGGAGGA 18
Wong,G.K.S., Deng,X.W. and Wang,J.
An analygis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80488576
                                                                                                                                                                                                                                                                                 1. .110
/organism="Oryza sativa (indica cultivar-group)"
/organism="Oryza sativa
/db xref="taxon:39946"
/clone lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'tissue type="whole animal"
'dev stage="egg"
'clone_lib="Nori Satoh unpublished cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV841732 Nori Satoh unpublished cDNA library, egg Ciona intestinalis cDNA clone rcieg05m22, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 10.2%; Score 25.8; DB 13; Length 110; 1 Similarity 60.9%; Pred. No. 2.5e+04; 42; Conservative 0; Mismatches 27; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.2%; Score 25.6; DB 7; Length 9 66.1%; Pred. No. 2.9e+04; ive 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                    Email: chenchen@genomics.org.cn
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                                                                                                                                                                                                                       Rice genomic sequence.
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37; Conservative (
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Ciona intestinalis
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Matches 37; Conserv
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                                                                                              1. .110
/organism="Cryza sativa (indica cultivar-group)"
/organism="Cryza sativa (indica cultivar-group)"
/mol_type="mcNA"
/cultivar="PA64s"
/db_xref="texon:39946"
/tissue_type="panicle"
/cell_type="sterile"
/dev_stage="heading/flowering"
/clone_lib="Cryza sativa cv. PA64s panicle sterile cDNA
library"
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
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The Genomes of Oryza sativa: A History of Duplications PLoS Biol. 3 (2), e38 (2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Bioinformatics Department
Hangahou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 110
PoLYA=No.
                                                              GI:58604032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 86-571-56805884
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yan Zhou
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                                                                                                                                                                                                 DU408432 1098474026684 CHORI-243 Ovis aries genomic clone CH243-202P18, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Blood"
/clone_lib="CHORL-243"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
The CHORL-243 sheep (M) (Ovis aries) BAC library produced
by Pieter de Jong's lab at CHORI
http://bacpac.chori.org/library.php?id=162"
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pecora; Bovidae; Caprinae; Ovie.

1 (bases 1 to 103)

2 (krkness 2 k. Shetty, J., de Jong, P., McEwan, J.C., Oddy, H. and Cockett, N.

2 (vine BAC End Sequences from Library CHORI-243

3 (byublished (2004)

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/strain="Texel breed"
/db_xref="taxon:9940"
/clone="CH243-202P18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Ovis aries"
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Zea mays
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Hominidae, Homo.

1 (bases 1 to 103)

Dias Neto, E., Garcia, R., Verjovski-Almeida, S., Briones, M.R.,

Brias Neto, B., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW800261 170400-203-e06 UM0060 Homo sapiens CDNA, mRNA sequence.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, Liliopaida; Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

( bases 1 to 117)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Reshick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Consortium for Maize Genomics
Unpublished (2002)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 GCGTGTCGCCCTGAGGTTTGAGGCCCAGACAGCTCGCAGGGCAGGGCCGGGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.2%; Score 25.6; DB 12; Length 117;
llarity 57.5%; Pred. No. 2.9e+04;
Conservative 0; Mismatches 34; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 10737800
                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: TR
Class: methylation filtered.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 CGATGTGAAGCTCCGGCCTC 25
                                                                                                                                                                                                                                                                                                                                                                        Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                        Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AGACGAGCGGCTCTGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW800261.1 GI:7852131
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Gaps

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33

GSS 24-JAN-2001

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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
CoRY, Site_2: BcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Library availability, please contact Pleter de Jong

(pdejong@mail.cho.org). Clones may be purchased from BACPAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end

page: http://ww.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 240 row: H column: 23

Seg primer: T7

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 108)
Akao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-240H23.TJ
                                                                                                                                                                                                                                                                       128 GCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCGGGCAGGGAGGCGGGGGAG 187
     /lab_host="DH10B"
/clome_lib="porcine skeletal muscle cDNA library (PoSM)"
/note="Organ: hind limbs; Vector: pSPORT1; Site_1: NotI;
Site_2: Sall:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Schurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPCI-23-240H23.TV RPCI-23 Mus musculus genomic clone RPCT-23-240H23, genomic survey sequence.
                                                                                                                                                                 Length 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
71: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                              9.9%; Score 25; DB 10;
56.8%; Pred. No. 4.2e+04;
iive 0; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
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/clone="RPCI-23-240H23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 bp
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/strain="C57BL/63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_lib="RPCI-23"
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                                                                                                                                                                                                                                                                                                                                                                            188 AGACGAGCGCCTCTGGCCCCT 208
                                                                                                                                                                                                                                                                                                                                                                                                                             30 AGGTGCGCACCCTGCCACCT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lab host="DH10B"
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                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                    Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS
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AZ697609/c
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AUTHORS
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KEYWORDS
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR2-UM0060-170 400-203-e06&t3=2000-04-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence start: 9
High quality sequence stop: 80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 bp mRNA linear EST 01-DEC-2005 POSM605016 F07R porcine skeletal muscle cDNA library (PoSM) Sus scrofa cDNA<sup>3</sup>, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                           /dev stage="Adult" | Clone lib="UM0060". | /Aclone lib="UM0060". | /Aclone lib="UM0060". | /Aclone lib="UM0060". | /Accession uterus; Vector: puc18; Site_1: Smal; Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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/dev stage="45 d and 90 d of gestation, birth, 7 wk and 1
yr o£ age"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 GGCCAGACAGCTCGCAGTCGGGCAGGGAGGGCGGGGAGAGACGAGGGGGCTCTGGCCCCT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 GGCCACACACTCGCGAACTGGGTGGAGCTGAGGGTGGAAGGGGAGTGGCACAGACCATC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ernst, C.W., Saama, P.M., Raney, N.E., Lin, S. and Roe, B.A. Sequencing of ESTs from a normalized porcine skeletal muscle cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.0%; Score 25.2; DB 7; Length 103; Best Local Similarity 55.8%; Pred. No. 3.76+04; Matches 48; Conservative 0; Mismatches 38; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michigan State University
B220 Anthony Hall, Bast Lansing, MI 48824, USA
Fat: 517 432 1941
Fax: 517 353 1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Ernst CW
Animal Science Molecular Genetics Lab
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                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 TAATTGTACTTCGGGCTCGTATTGTC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9823"
/sex="male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 crrcraragecageraacerrrere s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 100)
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                                                                                                                                                                                                                                           1. .103
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RESULT 12

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KEYWORDS

SOURCE

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CNS02660 110 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 240C22 of library G from Tetraodon nigroviridis, genomic survey
BZB36170 116 bp DNA linear GSS 18-MAR-2003
CH240_225C14.TJ CHORI-240 Bos taurus genomic clone CH240_225C14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL182961.
AL182961.1 GI:7821065
AL182961.1 GI:7821065
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Acanthomorpha, Acanthopterygii, Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="Blood"
/clone_lib="CHORL-240"
/note="Vector: pTARBACL.3; Site_l: Mbol; Site_2: Mbol;
Hereford bull il Domino 99375; CHORL-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.8%; Score 24.8; DB 12;
63.3%; Pred. No. 4.9e+04;
tive 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_225C14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                   genomic survey sequence.
                                                   BZ836170
BZ836170.1 GI:29063528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male
                                                                                                         Bos taurus (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                         Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
                                                                                         GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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VERSION
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CNS02660
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1. (Dases 1 to 89)

S. NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

High quality sequence stop: 19.

Location/Qualifiers

Location/Qualifiers
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                                                                                                                                                                                            BG718505 89 bp mRNA linear EST 08-MAY-2001
602696562F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4828574 5',
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                         Gaps
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                                                                         59 GCTTCTGTTTTCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCT 107
                                                                                             GCTTTCCTTTACTCTGCGCAGAGGCCTCAGGCTCCTTCTCACGCGGGCT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch
1 Similarity 57.9%; Pred. No. 4.78+04;
44; Conservative 0; Mismatches 32. TnAn1.
     DB 11; Length 108;
                                     15; Indels
 Score.25; DB 11;
Pred. No. 4.2e+04;
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 9.94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 GCGGAGGGTAGCCGCT
                                       34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .89
                                                                                                                                                                                                                                 mRNA sequence.
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Matches 44; Conserva
     Query Match
Best Local Similarity
Matches 34; Conserv
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DEFINITION
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TITLE
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BZ836170
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FEATURES

DRIGIN

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Gaps

Length 116;

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Search completed: October 16, 2006, 14:16:38 Job time : 2288 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-APP-2000) Genoscope - Centre National de Sequencage : Submitted (12-APP-2000) Genoscope - Centre National de Sequencage : PP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                     Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Sautin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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I (bases I to 107)

Virgin,S., Tianxiang,S., Karet,S., Wobus,C., Lay,M., Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Pheishing,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R., Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
                                       , Bouneau, L., Fisher, C.,
                                       Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenber, J. Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
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end : PUC-Ori"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Tetraodon nigroviridis"
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Pred. No. 4.9e+04;
Petradontoidea; Tetraodontidae; Tetraodon.
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Contact: Skip Virgin RNA Expression in Diseased Tissues by RDA RNA Expression in Diseased Tissues by RDA
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Best Local Similarity 52.0%;
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cloned into TA cloning vector (pre-cut vector pCR2.1-T0PO
was purchased from Invitrogen). Average insert size is
300bp. The insert also has same adaptor sequence on both
end. The sequence of the adaptor is:
5'-ATACGTGCAGGCTGATCTG -3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GCCCTTTGCTTCTGTTTTCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAG 110
                                                                                                                                                 Email: est@watson.wustl.edu
PCR products were directly cloned into TA cloning vector (pre-cut
vector pCR2.1-TOPO was prochased from Invitrogen). Average insert
size is 300bp. The insert also has same adaptor sequence on both
end. The sequence of the adaptor is: 5'-ATACGTGCAGGCTGGTTACATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGTGTTTCCCTTCTTTTTTTCGATGTTGATTCCATTTGCTTCCGATGGAGGAGTTCC
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TEL: 314 286 1800
Fax: 314 286 1810
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0
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                                                                                                                                                                                                                                                                                                                                                                               Seg primer: -40UP from Gibco.
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TYPE: DNA
CORGANISM: Homo sapiens
US-09-513-999C-16064
US-09-513-999C-16064
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US-09-210-305C-1
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Sequence 145, App
Sequence 145, App
Sequence 15065, A
Sequence 15065, A
Sequence 15067, A
Sequence 1377, A
Sequence 13, Appl
Sequence 13, Appl
Sequence 1, Appl
Sequence 2078, A
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15685, A
15277, A
13, Appl
1, Appl
20278, A
57, Appl
57, Appl
57, Appl
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Sequence 1, Appli
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                                                              October 16, 2006, 13:41:14 ; Search time 124 Seconds (without alignments) 3802.576 Million cell updates/sec
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Biocceleration Ltd.
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US-09-877-705A-145

US-09-877-705A-145

US-09-877-705A-145

US-09-513-999C-15065

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US-09-513-999C-29691

US-09-513-999C-29691

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        GenCore version (c) 1993 - 2006
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Maximum Match 100%
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Match
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Perfect score:
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Maximum DB
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Facent No. 6783961

GENERAL INFORMATION:

APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

TITLE OF INTENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT PILING DATE: 1999-02-24

FRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 16664

LENGTH: 92

LENGTH: 92

LENGTH: 92
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13592, A
16, Appl
20, Appl
7790, Ap
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Sequence 1, Application US/09210305C
Sequence 1, Application
Datent No. 6651010
GENERAL INPORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: A vector-based method for visualizing secondary structure of RNA molecules
                                                                                                               2856, Ap
2856, Ap
1, Appli
18431, A
8314, Ap
5830, Ap
3264, Ap
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2971, Ap
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PCT - US96 - 08014 - 34
US-08 - 905 - 223 - 68
US-10 - 131 - 821 - 2856
US-10 - 131 - 831 - 2856
US-08 - 362 - 454 - 1
US-09 - 621 - 976 - 18431
US-09 - 621 - 976 - 18431
US-09 - 621 - 976 - 18431
US-09 - 902 - 540 - 5830
US-09 - 913 - 924
US-09 - 533 - 335 - 335
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Pred. No. 3.6e+02;
0; Mismatches 17;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BACHMAN & LAPOINTE, P.C.
STREET: Suite 1201, 900 Chapel Street
CITY: New Haven
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-134-346A-45
US-08-976-288A-90
US-09-789-529-6
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9.8%;
Best Local Similarity 67.3%;
Matches 35; Conservative
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US-09-877-445/c
15-09-877-43A-145/c
5 Sequence 145, Application US/09877243A
7 Sequence 145, Application US/09877243A
7 Patent No. 6696256
6 GENERAL INFORMATION:
7 TILLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
7 TITLE OF INVENTION: TRANSCRIPTION FACTORS
7 TITLE OF INVENTION: TRANSCRIPTION FACTORS
7 CURRENT APPLICATION NUMBER: US/09/877,243A
7 CURRENT FILING DATE: 2001-08-16
7 NUMBER OF SEQ ID NOS: 162
7 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 AGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
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COUNTRY: U.S.A.
ZIP: 06510-2802
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23.8; DB 3; Dens.
Pred. No. 7e+02;
27; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
9.6%; Score 24.2; DB 3;
Best Local Similarity 43.5%; Pred. No. 5.6e+02;
Matches 30; Conservative 11; Mismatches 28;
                                                                      COMPUTER: IBM
COMPUTER: IBM
COMPUTER: IBM
COMPUTER: IBM
CONTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,305C
FILING DATE: 11-Dec-1998
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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Sequence 145, Application US/09877705A
Patent No. 6821737
GENERAL INPORMATION:
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nes 40; Conservative
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LENGTH: 78
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APPLICANT: Li, Jason

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TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPT
TITLE OF INVENTION: FACTOR ACTIVITY
FILE REPERROR: 26757-704
CURRENT APPLICATION NUMBER: US/09/877,705A
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 162
SOFTWARE PATENTIAL OF SEQ ID NOS: 162
LENGTH: 78
LENGTH: 78
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APPLICANT: Li, Jason
TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
TITLE OF INVENTION: TRANSCRIPTION FACTORS
FILE REFERENCE: 26757-701
CURRENT APPLICATION NUMBER: US/09/877,738C
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 162
SOFTMARE: PREENTIN VERSION 3.1
SEQ ID NO 145
LENGTH: 78
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APPLICANT: Duclert, A.
APPLICANT: Gordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961.
FILE REFERENCE: 59.US2.REG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Hybridization probe MP74
US-09-877-705A-145
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US-09-877-738C-145
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; Sequence 145, Application US/09877738C
; Patent No. 6924113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 59.73
Matches 40; Conservative
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APPLICANT: PENN, SIBATON G.
APPLICANT: PENN, SIBATON G.
APPLICANT: HANK, David R.
APPLICANT: GHEN, Wensheng
APPLICANT: GHEN, Wensheng
TITLE OF INVENTION: MYGSIN-IKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: WORDER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-27
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PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
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0
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9.0%; Score 22.6; DB 3; Length 66;
Best Local Similarity 64.2%; Pred. No. 1.5e+03;
Matches 34; Conservative 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 GCGTGGGGCCCCGGGGGATCGAGGCATCCAGCACAGAGGCGGCCAG 13
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR PPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 15065
LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-866-108A-15685/c
; Sequence 15685, Application US/09866108A
; Patent No. 6686188
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.6
Matches 32; Conservative
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APPLICANT: JI, Yonggang
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                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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WS-09-513-999C-23785

Sequence 23785, Application US/09513999C

Patence 23785, Application US/09513999C

Patence 23785, Application US/09513999C

Patence 23785, Application

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 678361

FILE REPERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 1999-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: PAtent.pm

SEQ ID NO 23785

LENGTH: 119
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APPLICANT: Duclett, A. J. B.
APPLICANT: Duclett, A. J. B.
APPLICANT: Duclett, A. J. T.
ITILE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT FAPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 1999-0-2-4
PRIOR PILING DATE: 1999-0-2-6
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Parent.pm
SEQ ID NO 15277
LENGTH: 67
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62 CTGTGCCCCACACCACCGCCTTCTTTCCAGATCCAGGGTCTCCAGGAGCTC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 CAGCTCGCAGTCGGGCAGGGCGGGGGAGAGACGAGCGGCTCTGGCCC 206
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Pred. No. 2.1e+03;
0; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-513-999C-15277
; Sequence 15277, Application US/09513999C
; Patent No. 6783961
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Best Local Similarity 53.4%;
Matches 47; Conservative (
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; ORGANISM: Homo sapiens
US-09-513-999C-15277
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ORGANISM: Homo sapiens
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US-09-347-613C-13/c
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86 CTGACTCCCTCTGCCACGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCC 138

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Query Match
Best Local Similarity 64.7*
Matches 33; Conservative
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CRGANISM: Homo sapiens
US-09-513-999C-20278
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-662-183A-13
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US-09-367-927A-1
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APPLICANT: Johansen, Teit E.
APPLICANT: Johansen, Teit E.
APPLICANT: Blom, Nikolaj
APPLICANT: Blom, Nikolaj
APPLICANT: Blom, Nikolaj
APPLICANT: Halesn, Claus
TITLE GF INVENTION: No. 6734284el Neurotrophic Factors
TITLE REFERENCE: 19313-001 DIV
CURRENT APPLICATION NUMBER: USO/9/662,183A
CURRENT APPLICATION NUMBER: USO/09/62,183A
CURRENT APPLICATION NUMBER: USO/09/62,183A
CURRENT APPLICATION NUMBER: USO/09/62,183A
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: USON 60/097,774
PRIOR APPLICATION NUMBER: USON 60/103,908
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-10-06
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                                                                             APPLICANT: JOHANSANION:
APPLICANT: Blom, Nikolaj
APPLICANT: Blom, Nikolaj
APPLICANT: Blom, Nikolaj
APPLICANT: Hansen, Claus
APPLICANT: Hansen, Claus
TITLE OF INVENTION: No. 65931333el Neurotrophic Factors
FILE REFERENCE: NeuroSearch 19313-001
CURRENT APPLICATION NUMBER: US/09/347,613C
CURRENT FILING DATE: 1998-07-06
FRIOR FILING DATE: 1998-07-06
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-25
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PRIOR PLING DATE: 1998-10-05
PRIOR PLING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 43
SEGFWARE: Patentin Ver. 2.1
Sequence 13, Application US/09347613C
Patent No. 6593133
GENERAL INFORMATION:
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US-09-347-613C-13
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US-09-662-183A-13/c
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LENGTH: 102
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FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT APPLICATION NUMBER: US 60/122,487
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SCOTUMARE: Patent.pm
SEQ ID NO 20278
LENGTH: 115
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8.8%; Score 22.2; DB 3; Length 115;
Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23; Indels
      Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09367927A

Patent No. 6300126

GENERAL INFORMATION:
APPLICANT: GRUMAT; INGRID
APPLICANT: RAINWRG, MITTLERER
APPLICANT: GRUMAT, ERIBERICK
APPLICANT: GRUMAT, ERIBERICK
APPLICANT: VAN DER VOGELWEIDE STRASSE, WALTHER
TITLE OF INVENTION: EXPRESSION OF FOR THE PERMANENT
TITLE OF INVENTION: EXPRESSION OF FOREIGN DNA
FILLE REFERENCE: 35280043USON
CURRENT APPLICATION NUMBER: US/09/367,927A
CURRENT FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 3.0
Query Match 8.8%; Score 22.2; DB 3; Length 1 Best Local Similarity 61.0%; Pred. No. 2.4e+03; Matches 36; Conservative 0; Mismatches 23; Indels
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US-09-513-999C-20278/c
; Sequence 20278, Application US/09513999C
; Patent No. 6783961
; GENERAL INPORMATION:
; APPLICANT: Dumag Milne Edwards, J.B.
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Search completed: October 16, 2006, 13:43:27 Job time : 125 secs
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63 GGGTGGGGGCGCCCCGGGAGAGACAGCACCTCGCAGCCCCAGAATTTGTTTTCGCTTTCG
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                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: GOLD, LARRY M.
APPLICANT: TUERK, CRAIG
TITLE OF INVENTION: METHOD OF SELECTING NUCLEIC
TITLE OF INVENTION: ACIDS ON THE BASIS OF
TITLE OF INVENTION: STRUCTURE
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: R400 B. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-442-062-57/c
; Sequence 57, Application US/08442062
; Settlence 57, Application US/08442062
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY M.
; APPLICANT: TUERK, CRAIG
; TITLE OF INVENTION: METHOD OF SELECTING NUCLEIC
; TITLE OF INVENTION: ACIDS ON THE BASIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZUDNITER READABLE FORM:

MEDIUM TYPE: Disketter, 3 1/5 inch, 1.44 MB
COMPUTER: IBM compatible
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordferfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/964,624D
FILING DATE: 21-OCTOBER-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/114,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: BAITY J. SWAIDSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEXOS
TELECOMMULICATION:
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US-07-964-624D-57/c
; Sequence 57, Application US/07964624D
; Patent No. 5496938
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TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: S7:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 TTTGAGGCCAGAC 156
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-964-624D-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Englewood
STATE: Colorado
COUNTRY: USA
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84 CTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGG 143
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TITLE OF INVENTION: STRUCTURE
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STRYEE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PELING DATE:
PRIOR: APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
CLASSIFCATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/14,131
FILING DATE: 10-UINE-1991
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: 11-UINE-1990
ATTORNEY/AGENT INFORMATION:
NAME: BATTY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEXOS/D1
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 TTTGAGGCCAGAC 156
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Sequence 16551, A
Sequence 16551, A
Sequence 12327, Ap
Sequence 17677, A
Sequence 145, App
Sequence 145, App
Sequence 145, App
Sequence 145, App
Sequence 145, App
Sequence 145, App
Sequence 6323, Ap
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(without alignments)
3804.035 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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6 US-11-173-902-22
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Maximum Match 100%
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252
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Match Length DB
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seq length: 120
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Maximum DB
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Sequence 192, App
Sequence 16455, A
Sequence 15685, A
Sequence 13685, A
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Sequence 13, Appl
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Sequence 21889, A
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US-10-918-95-37

US-10-918-95-37

US-10-918-95-37

US-10-918-95-37

US-10-918-95-37

US-09-918-063-33

US-09-918-063-33
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Sequence 16611, Application US/10310914A

Publication No. US20060003322A1

REBREAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01

CURRENT PAPLICATION NUMBER: US/10/310, 914A

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SEQ ID NO 16611

LENGTH: 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 caacccrccccaaaaaaacccaccrcccrccr 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 22, Application US/11173902; Publication No. US20060057611A1
; GENERAL INFORMATION:
APPLICANT: KAO, H. PIN
; APPLICANT: LAO, KAI QIN
; APPLICANT: JONES, ROBERT
; TITLE OF INVENTION: LOG-LINEAR AMPLIFICATION
; FILE REPERRENCE: 375461-021US
; CURRENT APPLICATION NUMBER: US/11/173,902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 GGAGGCGGGGGAGAGACGAGCGGCTCTGGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-310-914A-16611
                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
ORGANISM: Human
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| GENERAL INFORMATION:
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| APPLICANT: Endege, Wilson |
| APPLICANT: Endege, Wilson |
| APPLICANT: Endege, Wilson |
| APPLICANT: Endege, Wilson |
| APPLICANT: Monahan, John |
| APPLICANT: Monahan, John |
| APPLICANT: MOUSE GENES, COMPOSITIONS, KITS, AND METHODS FOR |
| TITLE OF INVENTION: HUMAN PROSTATE CANCER |
| TITLE OF INVENTION: HUMAN PROSTATE CANCER |
| TITLE OF INVENTION: HUMBER: 09/185,276 |
| PRIOR APPLICATION NUMBER: 09/185,276 |
| PRIOR APPLICATION NUMBER: 06/189,862 |
| PRIOR APPLICATION NUMBER: 06/189,862 |
| PRIOR APPLICATION NUMBER: 06/219 |
| PRIOR FILING DATE: 2000-03-16 |
| PRIOR PEPLICATION NUMBER: 06/21,314 |
| PRIOR APPLICATION NUMBER: 06/21,314 |
| PRIOR PEPLICATION NUMBER: 06/219,007 |
| PRIOR PILING DATE: 2000-06-09 |
| PRIOR PILING DATE: 2000-07-18 |
| PRIOR PILING DATE: 2000-07-18 |
| PRIOR APPLICATION NUMBER: 06/219,007 |
| PRIOR PILING DATE: 2000-07-18 |
| PRIOR PILING DATE: 2000-07-18 |
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| PRIOR PILING DATE: 2000-07-18 |
| PRIOR APPLICATION NUMBER: 06/219,007 |
| PRIOR PILING DATE: 2000-07-18 |
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Publication No. USZ0040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Monshan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MAI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR FILING DATE: 2003-02-16
42 CTGAGTTTTCAGGCAGGCAGGCAGGCAGGCAGGCAGGTAGGAGTACAGCAC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3158, Application US/10357930 Publication No. US20040259086A1 GENERAL INFORMATION:
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Matches 45; Conserv
                                                                                                                                                       198 CT 199
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US-10-357-930-3158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 TCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGGCTCCAGGTTCG 128
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; Publication No. US20040197797A1
; GENERAL INFORMATION:
; APPLICANT: INONGO, Hidetoshi
; APPLICANT: TANTION:
; TILLE OF INVENTION: GENER MAPPING METHOD USING MICROSATELLITE
; TILLE OF INVENTION: GENER WAPPING METHOD USING MICROSATELLITE
; TILLE OF INVENTION: GENER WAPPING MERRS
; FILE REPERENCE: ORIN-003C1P;
; CURRENT FILING DATE: 2003-09-26
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR PILING DATE: 2000-04-13
; PRIOR FILING DATE: 2000-04-13
; PRIOR FILING DATE: 2000-04-13
; PRIOR PILING DATE: 2002-29-28
; PRIOR FILING DATE: 2002-29-28
; PRIOR APPLICATION NUMBER: JP2002-3327516
; RIOR APPLICATION NUMBER: JP2002-332869
; RIOR APPLICATION NUMBER: JP2002-323869
; RIOR APPLICATION NUMBER: JP2002-323869
; RUMBER OF SEQ ID NOS: 27110
; LEMCTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-173-902-22
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Pred. No. 7.8e+02;
0; Mismatches 28; Indels
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CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION WUMBER: 60/584,665
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.3
SEQ ID NO 22
LENGTH: 96
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Best Local Similarity 60.0%;
Matches 42; Conservative
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ORGANISM: Artificial Sequence
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US-09-877-705A-145/c
US-09-877-705A-145/c
Sequence 145, Application US/09877705A
Sequence 145, Application US/09877705A
Sequence 145, Application VS-030008283A1
GENERAL INFORMATION:
APPLICANTION:
APPLICANT: Li, Jason
TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPY
TITLE OF INVENTION: PACTOR ACTIVITY
FILE REFERENCE: 26757-704
CURRENT APPLICATION NUMBER: US/09/877,705A
CURRENT PILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 145
LIBIGATH. 78
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17067, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

APPLICANT: Biller, Kvuzat

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUSO1

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 17067
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                                                                                                                   96 CTGCCACGGGTTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGA
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                                                                Gaps
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                Length 105;
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                                                                Indels
          Query Match
9.6%; Score 24.2; DB 6;
Best Local Similarity 53.7%; Pred. No. 1.6e+03;
Matches 44; Conservative 0; Mismatches 38;
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; OTHER INFORMATION: Hybridization probe MP74
US-09-877-705A-145
                                                                                                                                                                                                                    156 CAGCTCGCAGTCGGGCAGGGAG 177
                                                                                                                                                                                                                                                                       84 CATGGCGGGCAGGACGGGGG 105
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US-10-310-914A-17067
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Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 GGAGGGGGGGAGAGACGAGCGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24.6; DB 9;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.8%; Sco. 57.0%; Pred. No. 1...
57.0%; Pred. No. 1...
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR PELING DATE: 2000-02-17
PRIOR PELING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-12-13
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEO ID NOS: 62232
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 12327
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PRIOR APPLICATION NUMBER: PCT/USO0/26524
PRIOR PILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR PILING DATE: 1999-09-29
PRIOR PILING DATE: 1999-11-03
PRIOR PILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
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LOCATION: (28). (28)
LOCATION: (28). (28)
NAME/KEY: misc_feature
LOCATION: (40). (40)
OTHER INFORMATION: n equals a,t,g, o:
NAME/KEY: misc_feature
LOCATION: (53). (53)
OTHER INFORMATION: n equals a,t,g, o:
NAME/KEY: misc_feature
LOCATION: (72). (72)
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (77) ... (77)
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US-10-106-698-3252
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US-10-357-930-12327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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US-10-106-698-3252
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SEQ ID NO 3252
LENGTH: 105
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APPLICANT: Li, Jason
TITLE OF INVENTION: METHOD FOR IDENTIFYING A DISEASE STATE BASED ON A DETECTED MIXTURI
TITLE OF INVENTION: MCTIVATED TRANSCRIPTION FACTORS
FILE REFERENCE: 2675-703
CURRENT APPLICATION NUMBER: US/09/877,403A
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin version 3.1
SEQ ID NO 145
LENGTH: 78
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TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACTOF
FILTE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACTOF
FILE REFERENCE: 26757-702.301
CURRENT APPLICATION NUMBER: US/10/779,595
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 09/877,243
PRIOR PILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 162
SOFTWARE PATENTIN VERSION 3.1
SEQ ID NO 145
LENGTH: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Hybridization probe MP74
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                                                                                                                                                 RESULT 11
US-09-877-403A-145/c
; Sequence 145, Application US/09877403A
; Publication No. US20040214166A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-779-595-145/c
; Sequence 145, Application US/10779595
; Publication No. US20040132090A1
; GENERAL INFORMATION:
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169 GGCAGGG 175
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APPLICANT: Li, Xianqiang
TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS
FILE REPERENCE: 2675-705
CURRENT APPLICATION NUMBER: US/09/947,274
CURRENT APPLICATION NUMBER: US/09/947,274
FRIOR APPLICATION NUMBER: US/09/977,738
PRIOR FILING DATE: 2000-06-08
PRIOR PELING DATE: 2000-06-08
PRIOR FILING DATE: 2000-06-08
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US-09-877-738A-145/C
US-09-877-738A-145/C
Squence 145, Application US/09677738A
Publication No. US20030022173A1
GENERAL INFORMATION:
APPLICANT: L1, Jason METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
TITLE OF INVENTION: TRANSCRIPTION PACTORS
FILLE REFRENCE: 25/57-701
CURRENT APPLICATION NUMBER: 2001-06-01
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTING DATE: 2001-06-01
SSQ ID NO 145
LENGTH: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Hybridization probe MP74
US-09-947-274-145
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                                                                                                                                                    ; Sequence 145, Application US/09947274; Publication No. US20030017499A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial seguence
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   18 GTCAGAG 12
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Matches 40; Conserv
                                                                                                                          -09-947-274-145/c
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APPLICANT: Alexander
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APPLICANT: Alexander
APPLICANT: Coriza Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Headmaclogical Malignancies
FILE REPRENCE: 014058-0135208
FILE REPRENCE: 014058-0135208
GURRENT APPLICATION NUMBER: US 60/120,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR PELING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR PELING CONTE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PELING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,094
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,094
PRIOR APPLICATION NUMBER: US 60/202,046
PRIOR APPLICATION NUMBER: US 60/202,046
PRIOR PRILING DATE: 2000-08-03
PRIOR PRILING DATE: 2000-08-03
PRIOR PRILING DATE: 2000-08-03
PRIOR PRILING DATE: 2000-08-03
PRIOR PRILING DATE: US 000-08-03
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60.0%; Pred. No. 3e+03;
tive 0; Mismatches 26; Indels
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6323
LENGTH: 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0%
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
US-09-796-692-6323
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                                                                                                                                 sequence 1, Application US/10781499
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sequence 1, Application No. US20050054060A1
sequence 1. Application No. US20050054060A1
sequence 1. Application No. US20050054060A1
sequence 2. TITLE OF INVENTION: Method for the preparation of an evolved microorganism for the craft ITLE OF INVENTION: or modification of metabolic pathways
rithe OF INVENTION: or modification of metabolic pathways
rithe OF INVENTION: or modification of an evolved microorganism for the craft ITLE OF INVENTION: or modification of metabolic pathways
rithe OF ILLING DATE: 2003-02-18
sprior APPLICATION NUMBER: FR 0305769
sprior APPLICATION NUMBER: FR 0305769
sprior APPLICATION NUMBER: FR 0313054
sprior RILING DATE: 2003-05-14
sprior RILING DATE: 2003-10-6
sprior APPLICATION NUMBER: FR 0313054
sprior APPLICATION NUMBER: FR 0313054
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sprior FILING DATE: 2003-11-06
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION DIAGNOSIS AND THERAPY
FILE REPERBNCE: 2077.001200.
CURRENT FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PLING DATE: 2000-05-01
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; Sequence 6323, Application US/09796692
; Fublication No. US20020198362A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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; OTHER INFORMATION: DmetER
US-10-781-499-1
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Query Match 9.3%; Score 23.4; DB 6; Length 120;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 39; Conservative 0; Mismatches 26; Indels 0; Gaps
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Search completed: October 16, 2006, 13:57:18 Job time : 815 secs

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APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: COHEN, EDWARD H.
APPLICANT: ROCKEY, KRISTIN L.
APPLICANT: ROCKEY, KRISTIN L.
APPLICANT: HOBT, RENE
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
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Sequence 82, Appl
Sequence 3264, Ap
Sequence 424752,
Sequence 2971, Ap
Sequence 90, Appl
Sequence 90, Appl
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Published Applications NA New:*

| ENC Celerra SIDS3/prodata/2/pubpna/US09 NEW PUB. seq:*
| ENC Celerra SIDS3/prodata/2/pubpna/US06_NEW_PUB. seq:*
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| ENC Celerra SIDS3/prodata/2/pubpna/US1 NEW PUB. seq:*
| ENC Celerra SIDS3/prodata/2/pubpna/US11 NEW PUB. seq:*
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US-11-134-055-199

US-11-194-055-199

US-11-194-055-199

US-11-194-055-199

US-11-169-140-46

US-11-169-140-47

US-11-344-44

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US-11-244-330A-888
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                                       GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
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υ υ	3 18	7	47		US-11-370-584-612	Sequence	612, App	
'nΫ	4.18		51		US-11-143-642-1090	Sequence	1090, Ap	
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Ö	8 18	7	103		US-11-266-748A-413307	Sequence		
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					ALIGNMENTS			
RESULT US-11-	RESULT 1 US-11-043-824-258/c	-258/c						
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GEN	ERAL INFO	GENERAL INFORMATION: APPLICANT: Compugen	Ltd					
HI.	TLE OF IN	NVENTION: NVENTION:	NOVEL 1	SIG SIG	TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF CARDIAC DISEASE		AND ASSAYS AND METHODS	ID METHODS
II.	LE REFERI	ENCE: 184	7.1007 NIMBER	Ï	FILE REFERENCE: 1847.1007 CTERRENT APPLICATION NIMBER: 11S/11/043.824			
88	RRENT FII	CURRENT FILING DATE:	2005-01-	-0	-27			
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, ii i	LENGTH: 102	02						
·.	TYPE: DNA ORGANISM:	TYPE: DNA ORGANISM: Artificial	1,					
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QQ	26	GTCCGAGACACTTTCTCCAGGTTTG	CACTTTC	_5 _5	. AGGTTTGC 1			
RESULT US-11-	RESULT 2 US-11-365-556-82	-82						
	uence 82, lication	Sequence 82, Application US/11365 Publication No. US20060166252A1	tion US, 06016629	/11 52A	365556 1			
23.	EKAL INFO	OKMATION:		r				

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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
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US-11-266-748A-424752
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Sequence 3264, Application US/11370584

Publication No. US20060177863A1

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chen, Daniel
TITLE OF INVENTION: Biallalic markers for use in constructing a high
TITLE OF INVENTION: Biallalic markers for use in constructing a high
TITLE OF INVENTION: Biallalic across to the constructing a high
TITLE OF INVENTION: Biallalic across to the constructing a high
TITLE OF INVENTION: Biallalic across to the constructing a high
TITLE OF INVENTION: Biallalic across to the constructing a high
TITLE OF INVENTION: Biallalic across to the constructing a high
TITLE OF INVENTION: Biallalication NUMBER: US/03-08

PRIOR FILING DATE: 2003-01-21

PRIOR FILING DATE: 1999-10-20

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1998-11-23

PRIOR FILING DATE: 1998-11-23

PRIOR FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 3264

SEQ ID NO 3264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 TTTTCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 rerecergaagergagererergiekergeegagagagegeegegararracrereege 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 8.4%; Score 21.2; DB 9; Length 98;
1 Similarity 60.3%; Pred. No. 6.5e+03;
35; Conservative 0; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.3%; Score 21; DB 7; Length 47; Best Local Similarity 91.3%; Pred. No. 5.8e+03; Matches 21; Conservative 1; Mismatches 1; Indels
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FILE REFERENCE: DYAX/002
CURRENT APPLICATION NUMBER: US/11/365,556
CURRENT FILING DATE: 2006-02-28
FRIOR APPLICATION NUMBER: US/09/837,306
PRIOR FILING DATE: 2001-04-17
PRIOR PILING DATE: 2000-04-17
PRIOR PILING DATE: 2000-04-17
SPRIOR FILING DATE: 2000-04-17
SOFTWARE: PALENT NOS: 428
SOFTWARE: PALENT NOS: 2.1
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US-11-266-748A-424752/c
US-11-266-748A-424752/c
; Sequence 424752, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 GCAGGGAGGCCGGGGAGACG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 GCAGGAGGCGAGGAGAGACG 20
                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 35; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: 24
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Gaps
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APPLICANT: MILLIGAN, KARI
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
8.3%; Score 21; DB 8; Length 103
Best Local Similarity 66.7%; Pred. No. 7.5e+03;
Matches 30; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-266-748A-307408
; Sequence 307408, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
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128 GCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCGGGCAGGGAAGGCCGGGGGA 186
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59.3%; Pred. No. 1e+04;
tive 0; Mismatches 24; Indels
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8.2%; Score 20.6; DB 6; Length 100;
Best Local Similarity 59.3%; Pred. No. 9.8e+03;
Matches 35; Conservative 0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (1319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR FILING DATE: 2004-11-03
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PRIOR PILING DATE: 2005-01-14
PRIOR PILING DATE: 2005-01-16
PRIOR PILING DATE: 2005-01-16
PRIOR PILING DATE: 2005-01-16
PRIOR PILING DATE: 2005-01-16
PRIOR PILING DATE: 2005-01-16
PRIOR PILING DATE: 2005-01-16
PRIOR PILING DATE: 2005-01-18
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PRIOR PILING DATE: 2005-01-18
PRIOR PILING DATE: 2005-01-18
PRIOR PILING DATE: 2005-01-18
PRIOR PILING DATE: 2005-01-18
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-01-18
PRIOR PILING DATE: 2005-01-18
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-01-18
PRIOR PILING DATE: 2005-01-18
PRIOR PILING DATE: 2005-01-18
PRIOR PILING DATE: 2005-01-18
                                                          PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR PAPLICATION NUMBER: US 08/976,288
PRIOR PLLING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/129,930
PRIOR PILING DATE: 1993-09-30
PRIOR FILING DATE: 1992-11-12
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PATCHIN VETSION 3.3
SEQ ID NO 90
CURRENT APPLICATION NUMBER: US/10/874,990B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 300647, Application US/11266748A; Publication No. US20060134663A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
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Best Local Similarity 59.33
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Primer US-10-874-990B-90
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CORGANISM: Homo Sapiens
US-11-266-748A-300647
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US-11-266-748A-300647/c
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Sequence 90, Application US/10874990B

Sequence 90, Application US/10874990B

Publication No. US20060216303A1

GENERAL INFORMATION:
APPLICANT: SOMANTA LIMITED
APPLICANT: GENERAL, Roberto L.
APPLICANT: CERIANI, Roberto L.
APPLICANT: PETERSON, Jerry A.
APPLICANT: PADLAN, Eduardo A.
TITLE OF INVENTION: FROCESSES AND PRODUCTS WITH MODIFIED ANTIBODIES OF HUMAN MILK FAITTINE OF INVENTION: GLOBULE SPECIFICITY
FILE REFERENCE: SOMA1140-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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| Sequence 2971, Application US/11370584
| Publication No. US20060177863A1
| GENERAL INFORMATION:
| APPLICANT: Cohen, Daniel
| APPLICANT: Chumakov, Ilya
| TILLE OF INVENTION: Biallelic markers for use in constructing a high
| TILLE OF INVENTION: Biallelic markers for use in constructing a high
| TILLE OF INVENTION: Biallelic markers for use in constructing a high
| TILLE OF INVENTION: Biallelic markers for use in constructing a high
| TILLE OF INVENTION: Biallelic markers for use in constructing a high
| TILLE OF INVENTION: Biallelic markers for use in constructing a high
| TILLE OF INVENTION: Biallelic markers for use in constructing a high
| TILLE OF INVENTION: Biallelic markers for US/020P1
| FRIOR FILING DATE: 2006-03-08
| PRIOR PILING DATE: 1999-04-21
| PRIOR APPLICATION NUMBER: US 60/109,732
| PRIOR FILING DATE: 1998-11-23
| PRIOR FILING DATE: 1998-11-23
| PRIOR FILING DATE: 1998-04-21
| PRIOR FILING DATE: 1998-04-21
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| PRIOR FILING DATE: 1998-04-21
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                                                                                                                                                                                                                                Gaps
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                                                                                                                                                      Length 106;
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                                                                                                                                                   Query Match
8.3%; Score 20.8; DB 8; Length 10
Best Local Similarity 55.6%; Pred. No. 8.7e+03;
Matches 40; Conservative 0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i LOCATION: 24

i OTHER INFORMATION: 99-21310-416 : polymorphic base A or G

US-11-370-584-2971
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8.2%; Score 20.6; DB 7;
Best Local Similarity 70.3%; Pred. No. 7.7e+03;
Matches 26; Conservative 1; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 TCCAGGTTCGCG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 GACTGATTACCG 86
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-307408
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ORGANISM: Homo Sapiens
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GREREAL INCURRANT CACCE, CATIO M.

APPLICANT: Callow:
APPLICANT: Callow:
APPLICANT: Callow, Chang-Gong
APPLICANT: Callow, Gevigen, A.
APPLICANT: Callow, Gevigen, A.
APPLICANT: Callow, Gevigen, A.
APPLICANT: Callow, Gevigen, A.
APPLICANT: Callow, Gevigen, A.
APPLICANT: Callow, Gevigen, A.
APPLICANT: Callow, Gevigen, A.
APPLICANT: Callow, Gevigen, A.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT CANCER-ASSOCIATED CHROMOSOMAL
TITLE OF INVENTION: Diagnosis and Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow, Geographic Callow,
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8.1%; Score 20.4; DB 8; Length 86;
Best Local Similarity 61.1%; Pred. No. 1.1e+04;
Matches 33; Conservative 0; Mismatches 21; Indels
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8.1%; Score 20.4; DB 8;
Best Local Similarity 61.1%; Pred. No. 1.1e+04;
Matches 33; Conservative 0; Mismatches 21;
                                  PRIOR FILING DATE: 2004-06-16
PRIOR APPLICATION NUMBER: 60/580,797
PRIOR FILING DATE: 2004-06-18
NUMBER OF SEQ ID NOS: 663
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 198
LENGTH: 86
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Publication No. US20060099150A1
GENERAL INFORMATION:
APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 277, Application US/11194055; Publication No. US20060105360A1; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/580,959
                                                                                                                                                                                                                                                                                                                                     TYPE: DNA; ORGANISM: Homo sapiens
US-11-194-055-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-194-055-277
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US-11-169-140-46/c
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                                                                                                                                          US-11-194-USS-199, Application US/11194055
Publication No. US20060105360A1
GENERAL INFORMATION:
APPLICANT: Carlo M.
APPLICANT: Carlo M.
APPLICANT: Claria, George, A.
APPLICANT: Claria, Sevignani
TITLE OF INVENTION: DAGNOSIS AND TREATMENT OF CANCERS WITH
TITLE OF INVENTION: DAGNOSIS AND TREATMENT OF CANCER-ASSOCIATED CHROMOSOMAL
TITLE OF INVENTION: DAGNOSIS AND TREATMENT OF CANCER-ASSOCIATED CHROMOSOMAL
TITLE OF INVENTION: PEATURES
FILE REFERRENCE: 3589-1018-008
CURRENT APPLICATION NUMBER: US/11/194,055
CURRENT APPLICATION NUMBER: 60/543,119
PRIOR PILING DATE: 2004-02-09
PRIOR PELING DATE: 2004-02-09
PRIOR PELING DATE: 2004-02-09
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PRIOR PELING DATE: 2004-02-09
PRIOR PELING DATE: 2004-06-18
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US-11-194-055-198

Sequence 198, Application US/11194055

Publication No. US20060105360A1

GENERAL INFORMATION:
APPLICANT: Croce, Carlo M.
APPLICANT: Claim, Chang-Gong
APPLICANT: Claim, Sevignani
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
TITLE OF INVENTION: MicroRNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
TITLE OF INVENTION: FEATURES
FILE REFERENCE: 3589-1018-008

CURRENT PILING DATE: 2005-07-29
PRIOR PILING DATE: 2005-07-29
PRIOR PILING DATE: 2004-02-09
PRIOR PILING DATE: 2004-02-09
PRIOR PILING DATE: 2004-02-09
PRIOR PILING DATE: 2004-02-09
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Gaps

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APPLICANT: HOUSTON, Lou, L.
APPLICANT: HOUSTON, Lou, L.
APPLICANT: HOUSTON, Lou, L.
APPLICANT: SHERIDAN, Philip, J.
APPLICANT: HAMEY, Steephen
APPLICANT: GLANN, Jacqueline, M.
APPLICANT: GLANN, Jacqueline, M.
APPLICANT: GLANN, Jacqueline, M.
APPLICANT: GLANN, Jacqueline, M.
APPLICANT: GLANN, Jacqueline, M.
APPLICANT: GLAPIN, Steven
TITLE OF INVENTION: BARRIERS
FILE REFERENCE: 1474-037-999
CURRENT APPLICATION NUMBER: US/11/169,140
CURRENT APPLICATION NUMBER: US 60/246,819
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/248,478
PRIOR APPLICATION NUMBER: US 60/248,478
PRIOR APPLICATION NUMBER: US 60/248,478
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-10-02
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SEQUENCE 64. Application No. US20060134103A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE
TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS
FILE REFERENCE: 057220/1301
CURRENT APPLICATION NUMBER: US/11/191,244
CURRENT APPLICATION NUMBER: US/11/191,244
SOUTHARE OF SEQ ID NOS: 114
SOUTHARE PATENTIN VET: 2.1
SEQ ID NO 64
LENGTH: 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8; Length 95;
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Pred. No. 1.5e+04;
0; Mismatches 25
                                                                                       GENERAL INFORMATION:
APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
APPLICANT: HOUSTON, Lou, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Best Local Similarity 58.3%;
Matches 35; Conservative
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APPLICANT: HOUSTON, Lou, L.
APPLICANT: SHERLDAN, Philip, J.
APPLICANT: SHERLDAN, Philip, J.
APPLICANT: HAWLEY, Stephen
APPLICANT: GLYNN, Jacqueline, M.
APPLICANT: CHAPIN, Steven
TITLE OF INVENTION: BARRIERS
FILE REFERENCE: 11474-037-999
CURRENT APPLICATION NUMBER: US/11/169,140
CURRENT FILING DATE: 2005-06-27
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CURRENT APPLICATION NUMBER: US/11/191,244
CURRENT FILING DATE: 2005-07-27
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 63
LENGTH: 80
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* OTHER INFORMATION: Description of Artificial Sequence: Primer
US-11-191-244-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2003-00-27
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/248,819
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-10-02
SEXITARE: PALENTH VERSION 3.0
SEQ ID NO 46
LENGTH: 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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US-11-191-244-63/c
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US-11-169-140-47/c
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